

Characterization of *Pseudomonas aeruginosa* phages for phage therapy

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Tiivistelmä — Referat — Abstract <p>Antibiotic-resistant bacteria are an increasing threat to global health, caused by the excessive use of antibiotics and the lack of new antimicrobial agents being introduced to the market. New approaches to prevent and cure bacterial infections are needed to halt the growing crisis. One of the most promising alternatives is phage therapy which utilizes bacteriophages to target and kill pathogens with specificity. <i>Pseudomonas aeruginosa</i> is a common opportunistic pathogen that is intrinsically resistant to antibiotics, making it one of the most heavily studied targets of phage therapy. In this study, I characterized four <i>P. aeruginosa</i> phages, fHo-Pae01, PA1P1, PA8P1 and PA11P1, and evaluate their potency in therapeutic applications.</p> <p>Bioinformatic analysis of the genomes revealed the phages to be genetically highly similar and belonging to the <i>Pbunavirus</i> genus of the <i>Myoviridae</i> family. No genes encoding harmful toxins, antibiotic-resistance, or lysogeny were predicted. On the other hand, many of the predicted genes had unknown functions. The host ranges of the phages were assessed using 47 clinical <i>P. aeruginosa</i> strains and predicted host receptor binding tail proteins were compared. Some correlation between the host ranges and mutations in the tail proteins were observed but this alone was not sufficient to explain the differences in the host ranges.</p> <p>The recently isolated vB_PaeM_fHoPae01 (fHo-Pae01) phage was further characterized by a one-step growth curve and imaged with a promising atomic force microscopy method that had not been used before in the Skurnik group. Though the imaging results failed to provide any further knowledge of the phage, the 70-minute-long latent period of infection could be determined from the growth curve. Anion-exchange chromatography was found inefficient in purifying the fHo-Pae01 phage, so alternative methods such as endotoxin columns should be used when purifying these phages for patient use.</p> <p>In conclusion, all four phages appeared to be safe for therapeutic use based on current knowledge, and PA1P1 and PA11P1 were the most promising candidates due to their broad host ranges.</p>	
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Tiivistelmä — Referat — Abstract <p>Antibioottiresistentit bakteerikannat ovat kasvava uhka kansanterveydelle. Tämä johtuu antibioottien ylenpalttisesta käytöstä nyky-yhteiskunnassa ja uusien antimikrobien yhdisteiden kehityksen huomattavasta hidastumisesta. Uusien bakteeri-infektioita parantavien ja ehkäisevien keinojen kehittäminen joko antibioottien tilalle tai rinnalle on välttämätöntä maailmanlaajuisen kriisin pysäyttämiseksi. Yksi lupaavimmista hoidoista on faagiterapia, jossa bakteeriofageja hyödynnetään patogeenisten bakteereiden hävityksessä.</p> <p><i>Pseudomonas aeruginosa</i> on yleinen opportunistinen patogeeni, joka on luontaisesti hyvin vastustuskykyinen antibiooteille. Tästä syystä sitä on tutkittu paljon faagiterapian kohteena. Tässä tutkielmassa karakterisoin neljä <i>P. aeruginosa</i> faagia - fHo-Pae01, PA1P1, PA8P1 sekä PA11P1 – ja arvioin niiden käyttökelpoisuutta terapeuttisissa sovelluksissa.</p> <p>Faagien genomit osoittautuivat hyvin samankaltaisiksi bioinformaattisessa analyysissä. Fylogeneettisesti samaa lajia edustavat neljä faagia luokiteltiin <i>Myoviridae</i>-perheen <i>Pbunavirus</i>-sukuun. Haitallisia toksineja, antibioottiresistenttiyttä tai lysogeniaa koodaavia geenejä ei havaittu. Toisaalta vain osalla faagien oletetuista geeneistä oli tunnistettava tehtävä. Faagien isäntäkirjoja tutkittiin 47 kliinisellä <i>P. aeruginosa</i> kannalla ja oletettuja isännän reseptoriin sitoutuvia häntäproteiineja vertailtiin keskenään. Tulokset osittain korreloivat toisiaan, mutta erot häntäproteiineissa eivät riittäneet selittämään eroja isäntäkirjoissa.</p> <p>Vastikään eristettyä faagia, fHo-Pae01, karakterisoitiin myös kasvukäyrän sekä AFM mikroskopian (atomic force microscopy) avulla. Kyseistä mikroskooppia ei ollut aiemmin käytetty Skurnikin ryhmässä eikä sen resoluutio riittänyt pienille faagikapsideille. Sen sijaan kasvukäyrästä kyettiin määrittämään infektion latentin vaiheen pituudeksi 70 minuuttia. Puhdistuksessa havaittiin, että anioninvaihtokromatografia ei ole riittävän tehokas keino puhdistaa fHo-Pae01 faagia. Vaihtoehtoisia keinoja kuten endotoksiinipylvästä on käytettävä, mikäli faagia halutaan puhdistaa terapiatuotteeksi.</p> <p>Kaikki neljä faagia vaikuttivat olevan turvallisia käytettäväksi faagiterapiassa. PA1P1 ja PA11P1 olivat lupaavimmat kandidaatit niiden laajemman isäntäkirjon johdosta.</p>	
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INTRODUCTION

Pseudomonas aeruginosa is a gram-negative, opportunistic pathogen occurring in the human intestine, on the skin, and in the environment. *P. aeruginosa* is pathogenic to humans only when introduced to an area lacking a natural defense mechanism or when a person's defenses are impaired due to an illness. Infection is often produced in damaged tissue such as wounds or burns [1], in the urinary tract after catheter introduction [2], or as a chronic respiratory infection in cystic fibrosis patients [3]. In addition, *P. aeruginosa* may in the most extreme cases cause fatal sepsis when invading the bloodstream. Among other *Pseudomonas* species, *P. aeruginosa* is naturally resistant to many antimicrobial agents [4] as well as to the immune system due to its biofilm formation [5,6].

Multidrug resistance of *P. aeruginosa* is occurring primarily in cystic fibrosis patients and patients hospitalized in intensive care units, and the proportion of isolates resistant to multiple drugs is rising rapidly [7]. The excessive use of antibiotics and the halt in the development of new antimicrobial drugs has caused the rise of antibiotic-resistance in bacteria and the selection for resistance genes [8].

Alternative ways to cure infections caused by antibiotic-resistant bacteria are being developed to replace or act alongside antibiotics. Phage therapy, a method which utilizes bacterial viruses (bacteriophages) to kill specific infectious bacteria, presents one possible way to battle the global threat caused by the spreading of antimicrobial-resistance [9,10]. Lytic phages lyse the bacterial cell at the end of their infection cycle, therefore killing the bacteria. This event lays the foundation for phage therapy [11]. The phages used for therapeutic purposes must meet strict criteria to be deemed safe to use. In addition to being free of any toxin or antibiotic-resistance coding genes they must be virulent, unable of lysogenic conversion [12]. A lysogenic phage integrates its genome into the host's chromosome becoming a prophage [11], usually making the host phage-resistant [11,12]. Lysogenic phages may convert back to a lytic cycle in certain conditions, but as a prophage, they do not cause cell lysis and thus would be ineffective in phage therapy [11]. Identifying lysogenic phages can often be carried out with genomic analysis, as the genomes of lysogenic phages usually code integrases, transposases or lytic phage repressors [13].

Over 94% of the known *Pseudomonas* phages found in the National Center for Biotechnology Information (NCBI) database are classified in three families of the *Caudovirales* order: *Podoviridae*, *Siphoviridae*, and *Myoviridae* with genome sizes ranging from 3.6 kb to 320 kb [14,15]. All phages in the order are double-stranded DNA viruses with differing tail structures, and approximately 60% of

them are lytic. The genome size is generally larger in *Myoviridae* than in *Podoviridae* or *Siphoviridae*, ranging from 64 kb to ~310 kb, whereas in the other two the size usually falls under 80 kb. It is characteristic of the phages in the *Myoviridae* family to have a long tail that contracts upon the phage injecting its genome into the host cell. [16]

This work aimed to study the genomic properties of four *P. aeruginosa* phages, in order to verify them safe to use for therapeutic purposes within the range of current knowledge. Additional experiments were conducted to determine the capsid structure and infection characteristics of one of the phages, vB_PaeM_fHoPae01 (fHo-Pae01, GenBank: MK318076.1), as it is a recent isolate of the Skurnik group.

MATERIALS AND METHODS

Phages, bacterial strains and growth conditions

All bacterial strains used in laboratory work were clinical *Pseudomonas aeruginosa* strains (HUSLAB, [17]) (Table S1).

The fHo-Pae01 phage was previously isolated in the Skurnik group by Tommi Patinen [18]. *P. aeruginosa* #5525 (HUSLAB) [18] was used as the standard host for this phage. Phages PA1P1, PA8P1 and PA11P1 were isolated elsewhere [17]. The standard hosts used were *P. aeruginosa* PA1 for PA1P1, PA8 for PA8P1, and PA11 for PA11P1 [17].

The bacterial cultures and phages were incubated at +37 °C using Luria broth (LB) liquid medium or soft agar medium (0.4% (w/v) agar) solidified on LB agar plates (1.5% (w/v) agar) [19]. The phage lysates were prepared from semiconfluent soft agar plates with the host bacteria from a culture incubated until the logarithmic growth phase. The amount of bacterial culture added was calculated from the equation: 25.5µl OD₆₀₀⁻¹. The same equation was used for the amount of bacterial culture when titrating phages on double layer plates [19].

In silico analysis of phage genomes

All phage genomes had previously been sequenced by next-generation sequencing (Eurofins GATC), assemblies of the over 12 million reads per genome had been made, and the contigs containing the phage genomes had been identified. In this work, PhageTerm program [20] was used to estimate the genome origins and packaging methods of the phages. The genomes were managed with Geneious 11.1.5 (<https://www.geneious.com>). The assembled genomes were also aligned in

Geneious 11.1.5 (<https://www.geneious.com>) with the original reads to ensure no mistakes were made in the assembly.

The preliminary annotations were automatically carried out with RAST 2.0 (Rapid Annotation using Subsystem Technology) [21-23]. Glimmer3 software [24,25] was used to make corrections to the annotations formed by RAST 2.0 [21-23]. Based on the RAST 2.0 [21-23] and Glimmer3 [24,25] results, the final, more detailed annotations were performed with BLASTp (Protein Basic Local Alignment Search Tool) [26], and the results were manually evaluated.

The phage genomes were screened for tRNA (tRNAscan-SE 2.0 [27], Aragorn [28]), virulence (VirulenceFinder 2.0 [29]), and antibiotic-resistance genes (ResFinder 3.1 [30]).

A comparative alignment between the phage genomes and the type phage PB1 (GenBank: NC_011810.1) genome was conducted with Geneious 11.1.5 (<https://www.geneious.com>), Geneious alignment tool.

A phylogenetic tree was constructed with VICTOR software (Virus Classification and Tree Building Online Resource) [31] using Genome-BLAST Distance Phylogeny (GBDP) method. Genome-wide BLASTN runs were performed to the four phages and the type phage PB1. 22 of the best matches (query cover >90%) were chosen for the tree (Table S2). The open reading frame (ORF) of the first predicted gene in fHo-Pae01, FHP001, was identified in all phage genomes used for the tree. All the genomes were then set to start from that ORF, to yield a more reliable phylogenetic tree.

A protein corresponding to a predicted tail fiber protein (GenBank: BAU20669.1) of *Pseudomonas* phage KPP22 (GenBank: LC105987.1), assumed to affect the adsorption of the phage to the host cell [32], was identified in the genomes of fHo-Pae01 (FHP062), PA1P1 (PA1P1_063), PA8P1 (PA8P1_062), and PA11P1 (PA11P1_062). The amino acid sequences of the predicted tail fiber proteins in fHo-Pae01, PA1P1, PA8P1, and PA11P1 were aligned with Clustal Omega 1.2.4 [33].

Host range screening

The host ranges for all four phages were screened with the 47 clinical, antibiotic-resistant *P. aeruginosa* strains available (Table S1). Screenings were performed in liquid cultures on a 96-well plate over 6 hours, by measuring the absorbance at 595 nm (Hidex Plate CHAMELEON Multilabel Detection Platform) at 60 min intervals. In each well, 190 μ l of 1:40 dilution of the host bacteria overnight culture was mixed with 10 μ l lysate (10^9 pfu/ml) of one of the phages. Wells with LB medium replacing the phage lysate were used as negative controls. As positive control, each phage

was also used to infect its standard host. The host range liquid culture screening method had previously been tested (Schaedig *et al.*, unpublished results) to yield results comparable to the more commonly used plating method [34].

One-step growth curve

The standard host of the phage fHo-Pae01, *P. aeruginosa* #5525, was incubated in 10 ml LB medium until the absorbance, measured with Cell density meter DSM-Micro (Laxco) at 600 nm was 0.4 – 0.5. The phage was added to reach an MOI value of 0.0005 to ensure no more than one phage would infect a single host cell. A 150 µl sample at 0 min was taken immediately. The sample was treated by first harvesting the cells by centrifugation for 1 min at 11,000 x g. Then, the supernatant was discarded and replaced by fresh media so that only the phages adsorbed on the surface or inside the cells were taken into account. The sample was then titrated.

The phages were left to adsorb for 15 min with light shaking, after which the cells were harvested by centrifugation for 5 min at 4,500 x g, and the media was replaced to produce a synchronized infection. A dilution series was prepared until 10^{-3} in 10 ml LB medium. The incubation was continued, and 20 – 50 µl samples titrated every 10 – 30 min.

The growth curve was calculated using the mean values of three separate experiments by assigning the value 1 to correspond the phage titer at 0 min. [35,36]

Phage purification with anion-exchange chromatography

The phage lysate was concentrated to a volume of 1 ml and changed to buffer A (20 mM Tris-Cl, pH 8.5) by ultrafiltration with a Vivaspın 6 (100 kDa) centrifugal PES membrane concentrator (Sartorius). The sample was then filtered through a 0.2 µm pore filter. The anion-exchange chromatography was performed with Äkta Purifier (GE Healthcare), and a CIMmultus QA-1 tube advanced composite column with a 6-µm pore size (BIA Separations). The high pH of 8.5 for the buffers was selected to ensure the negative charge of the major capsid protein. The isoelectric point of the putative major structural protein of fHo-Pae01, FHP_041, was determined using EMBOSS Pepstats software [37].

A linear gradient purification was made to determine the conditions for the two-step purification. The sample was injected to the column in buffer A, and the phage was eluted with buffer A and with a 0 mM – 550 mM gradient of NaCl. (Fig. S2)

In the step purification, the sample was injected to the column in buffer A, the column was washed with buffer A with 160 mM NaCl, and the phage was eluted with buffer A with 350 mM NaCl. The two fractions containing the phage were pooled, and the buffer was changed to gelatin-free SM buffer (100 mM NaCl, 10 mM MgSO₄, 50mM Tris-HCl, pH 7.5) with a Vivaspin 6 centrifugal concentrator. (Fig. S3)

Atomic force microscopy

The purified phage was imaged a multimode 8 AFM connected to a Nanoscope V controller (Bruker). The images were taken in tapping mode in the air with an E scanner using NCHV-A probes (Bruker AFM probes). The images were taken at Aalto University, Department of Bioproducts and Biosystems.

RESULTS

Genome analyses

The genomic sequences of PA1P1, PA8P1, and PA11P1 were sequenced previously. PhageTerm [20] software was then used to determine the physical ends of the pre-assembled genomes. A headful packaging mechanism was predicted by the program as the method used by all three phages to package their genome into the phage capsid. The mechanism does not have a specific cleaving site for the C terminal end of the genome, but rather cleaves the DNA strand once the virion head is full, resulting in genomes of varying lengths in individual phage particles [38,39]. The annotation and PhageTerm analysis of fHo-Pae01 was done by Pulkkinen *et al.* (manuscript under preparation).

All four phage genomes – fHo-Pae01, PA1P1, PA8P1, and PA11P1 – were similar in length (65 – 67 kbp) and GC content (55 – 56%). Furthermore, the number of predicted genes was 92 – 93 in all genomes, of which 66 – 67 were hypothetical proteins with unknown functions (Tables S3 – S6). The scans performed using tRNAscan-SE 2.0 [27], and Aragorn [28] found no transfer RNA coding genes. The phages were expected to be strictly lytic as no lysogeny-associated genes or integrases were identified. Additionally, no virulence-associated, toxic or antibiotic-resistance genes were recognized in any of the four genomes. (Table 1)

All genomic sequences were constructed using over 12 million sequencing reads. The genomes were aligned with the original reads to find mistakes made during the assembly. One uncertain sequencing result was found in all four genomes: a 9 – 10 bp guanine repeat in *PA1P1_61A*,

PA8P1_60A, and *PA11P1_60A*, and in between the predicted genes *FHP_059* and *FHP_060* in fHo-Pae01. The length of the repeat was nine bp in approximately half of the reads and ten bp in the other half. The final sequences have the sequence with nine guanine nucleotides in accordance to the sequence of PB1. The sequencing method may not have been sensitive enough to reliably be able to determine the length of unusually long one-nucleotide repeats.

Comparative genome analysis

Altogether, the genomes of fHo-Pae01, PA1P1, PA8P1, and PA11P1 were highly similar, sharing over 90% identities with each other, and 85 – 86% with the *Pbunavirus* type phage PB1 (Table 1). The pattern of predicted genes is also highly similar in all four phages and the type phage (Fig. 1) with the most significant differences described in Table 2.

The phylogenetic tree (Fig. 2) clustered the 27 phage genomes as seven species, all belonging to the *Pbunavirus* genus and *Myoviridae* family. The phages fHo-Pae01, PA1P1, PA8P1, and PA11P1, were classified as the same species as *Pseudomonas* phages 14_1, JG024, NP3, PII10A, SL1, and SN rather than the *Pbunavirus* type phage PB1.

Table 1: Statistic of fHo-Pae01, PA1P1, PA8P1, PA11P1, and the type phage PB1 genome analyses. Number of predicted genes and hypothetical proteins, GC content, genome length, and sequence identities of the phage genomes with each other.

	fHo-Pae01	PA1P1	PA8P1	PA11P1	PB1
Genome length (bp)	66,418	66,612	65,690	66,049	65,764
Predicted genes	92	93	92	92	94
Hypothetical proteins	66	67	67	67	80
GC%	55.7	55.8	55.7	55.7	54.9
Identity with fHo-Pae01 (%)	100	94.8	93.5	94.3	86.1
Identity with PA1P1 (%)	94.8	100	94.8	97.1	86.3
Identity with PA8P1 (%)	93.5	94.8	100	96.4	85.5
Identity with PA11P1 (%)	94.3	97.1	96.4	100	85.1

All statistics were calculated using Geneious 11.1.5 (<https://www.geneious.com>).

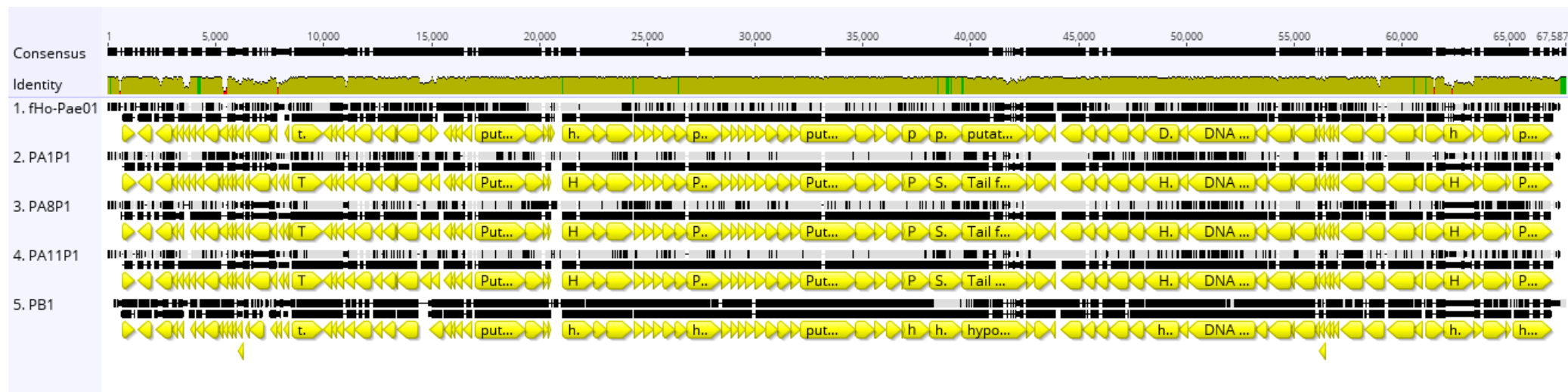


Fig. 1. A genome-wide alignment created with Geneious 11.1.5 (<https://www.geneious.com>) software of the fHo-Pae01 (GenBank: MK318076.1), PA1P1, PA8P1, PA11P1 and PB1 (GenBank: NC_011810.1) phage genomes. The predicted genes are marked in yellow. The height and color of the identity bar indicates the mean pairwise identity over all pairs in the column (Green: 100% identity, yellow: 30% - 100% identity, red: below 30% identity). The PB1 type phage shared an overall 85-86% identity with the other phage genomes. The identities among phages fHo-Pae01, PA1P1, PA8P1 and PA11P1 were even higher: 93-97%. The genome of PB1 was adjusted to originate from the gene corresponding to the first predicted gene in the other phage genomes.

Table 2: Major differences in the predicted genes of fHo-Pae01, PA1P1, PA8P1, PA11P1, and PB1.

fHo-Pae01	PA1P1	PA8P1	PA11P1	PB1	Description of the differences
<i>FHP_003c</i>	<i>PA1P1_003c</i>	<i>PA8P1_003c</i>	<i>PA11P1_003c</i>	<i>PB1_gp81</i>	PA1P1_003c, PA8P1_003c and PA11P1_003c are identical. FHP_003c and PB1_gp81 are similar to the previous three and to each other.
<i>FHP_006c</i>	<i>PA1P1_006c</i>	no seq	<i>PA11P1_006c</i>	no seq	
no seq	<i>PA1P1_011c</i>	no seq	no seq	<i>PB1_gp88</i>	
<i>FHP_013c</i>	<i>PA1P1_014c</i>	<i>PA8P1_012c</i>	<i>PA11P1_013c</i>	<i>PB1_gp91</i> , <i>PB1_gp92</i>	PB1_gp91 is a different protein than PB1_gp92, and both are different proteins than the others shown. FHP_013c is similar to PA1P1_014c.
<i>FHP_015c</i>	<i>PA1P1_016c</i>	<i>PA8P1_014c</i>	<i>PA11P1_015c</i>	<i>PB1_gp94</i>	PA8P1_014c and PA11P1_015c are identical but a different protein from the others shown. PB1_gp94 is approximately 90 amino acid residues shorter than FHP_015c and PA1P1_016c.
no ORF	<i>PA1P1_018c</i>	<i>PA8P1_016c</i>	<i>PA11P1_017c</i>	<i>PB1_gp02</i>	PB1_gp02 is a different protein from the others. A mutation in fHo-Pae01 leading to frameshift has caused a stop codon in the region.
<i>FHP_017c</i>	<i>PA1P1_019c</i>	<i>PA8P1_017c</i>	<i>PA11P1_018c</i>	<i>PB1_gp03</i>	PB1_gp03 is a different protein from the others.
no ORF	no ORF	<i>PA8P1_018</i>	no ORF	no ORF	Glimmer3 found a gene in this region of fHo-Pae01 and PA8P1. The gene predicted in fHo-Pae01 is similar to PA8P1_018, but it has not been annotated.
<i>FHP_026c</i>	<i>PA1P1_028c</i>	<i>PA8P1_027c</i>	<i>PA11P1_027c</i>	no ORF	Glimmer3 predicted a similar gene in PB1, but it has not been annotated. FHP_026c and PA1P1_030c are similar to the others shown and to one another.
<i>FHP_028c</i>	<i>PA1P1_030c</i>	<i>PA8P1_029c</i>	<i>PA11P1_029c</i>	no seq	
<i>FHP_029</i>	<i>PA1P1_031c</i>	<i>PA8P1_030c</i>	<i>PA11P1_030c</i>	<i>PB1_gp13</i>	PB1_gp13 is approximately 55 amino acid residues longer than the others shown, has a different predicted start codon, and is similar to PA1P1_031c, PA8P1_030c, and PA11P1_030c. FHP_029 is a different protein from the others shown.
<i>FHP_038</i>	no ORF	no ORF	no ORF	no ORF	Glimmer3 did not predict any genes. The DNA sequence has premature stop codons in all but FHP_038.

<i>FHP_084c</i>	<i>PA1P1_085c</i>	<i>PA8P1_084c</i>	<i>PA11P1_084c</i>	<i>PB1_gp69</i>	PA8P1_084c and PB1_gp69 are identical. The others are similar to them and to one another.
<i>FHP_088</i>	<i>PA1P1_089</i>	<i>PA8P1_088</i>	<i>PA11P1_088</i>	<i>PB1_gp73</i>	PA8P1_088 and PB1_gp73 are different proteins from the others and from one another. PA1P1_089 and PA11P1_088 are identical, and FHP_088 is similar to them.

Glimmer3 [24,25] and *BLASTp* [26] software were used to verify some of the genes predicted by *RAST 2.0* [21-23]. No seq: a gap in the sequence on the site of the predicted gene. No ORF: no annotated predicted gene on the site. Identical: 95 – 100% pairwise amino acid identity. Similar: 60 – 95% pairwise amino acid identity. Low amino acid identity: 45 – 60% pairwise amino acid identity. Different protein: less than 45% pairwise amino acid identity.

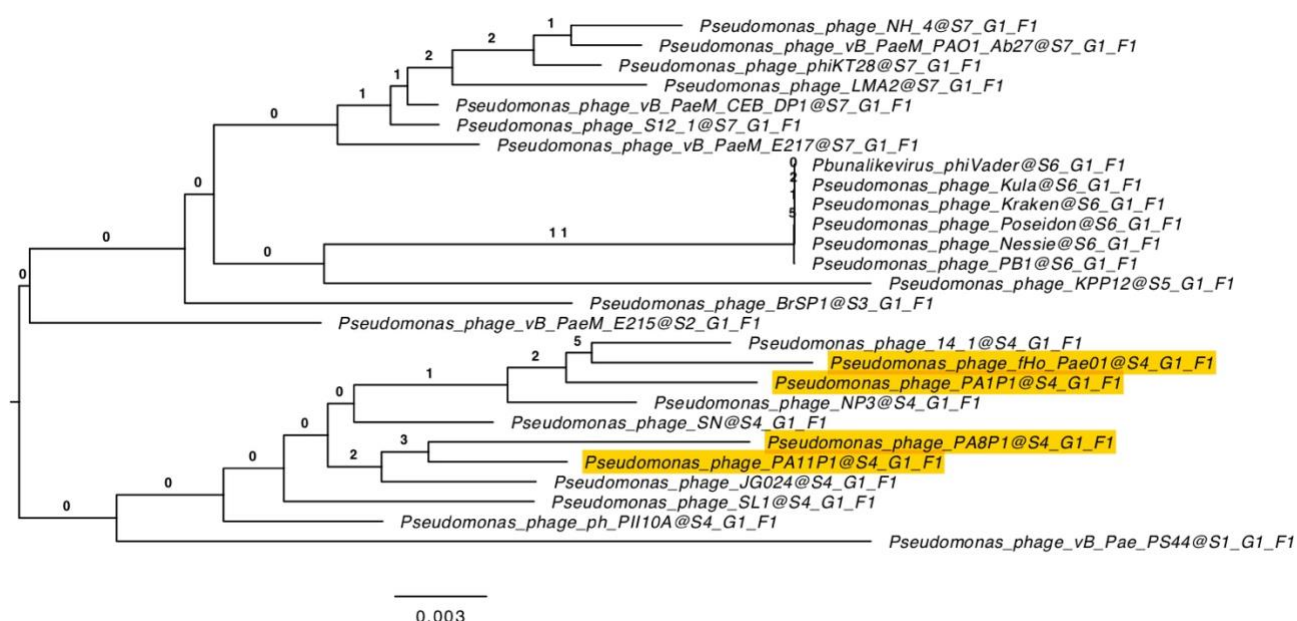


Fig. 2. A phylogenetic tree of the 17 closest BLASTn matches to the fHo-Pae01, PA1P1, PA8P1, and PA11P1 phage genomes (highlighted in yellow) and 5 closest BLASTn matches to the type phage PB1 phage genome. The tree was constructed with VICTOR (Virus Classification and Tree Building Online Resource) [31]. All of the genomes in the tree belong to Pseudomonas phage genus of the Myoviridae family. The genomes were clustered in 7 species. The phages fHo-Pae01, PA1P1, PA8P1 and PA11P1 are classified as the same species as Pseudomonas phages 14_1, JG024, NP3, PII10A, SL1, and SN, rather than Pseudomonas phage PB1 which is the type phage of the genus. S: species, G: genus, F: family.

Infection cycle

A one-step growth curve experiment was conducted to fHo-Pae01 to determine the number of new phage progenies released by a single infected bacterial cell (burst size), as well as the duration of the latent period, i.e., the time from infection to the beginning of cell lysis. The latent period was determined to be 70 minutes long. However, the four repeated experiments deviated substantially from one another later during the infection cycle. Thus, the burst size could not be determined.

Experiments with longer incubation time did not reveal a new latent period (data not shown). (Fig. 3)

Host range

The host ranges of all four phages were assessed using 47 clinical *P. aeruginosa* strains (Table S7, Fig. S1). Of the four phages, fHo-Pae01 had the narrowest specificity, infecting only 14 clinical strains (30%). PA1P1 infected 33 (70%), PA8P1 infected 24 (51%) and, PA11P1 infected 31 (66%) of the strains. A comparative alignment of the possible host receptor recognizing tail fiber proteins was performed to elucidate the differences in host specificities. According to the alignment (Fig. 4), the predicted tail proteins PA1P1_063 and PA11P1_062 were 100.00% identical. Moreover, PA8P1_062 was 97.40% identical to PA1P1_063 and PA11P1_062. However, the tail fiber protein of fHo-Pae01, FHP062, shared a sequence identity of 82.40% with PA1P1_063 and PA11P1_062, and 84.06% with PA8P1_062. The variation between FHP062 and the others was concentrated in the C termini of the proteins with a pairwise identity of 54.0% in A670 – A963 determined by Geneious 11.1.5.

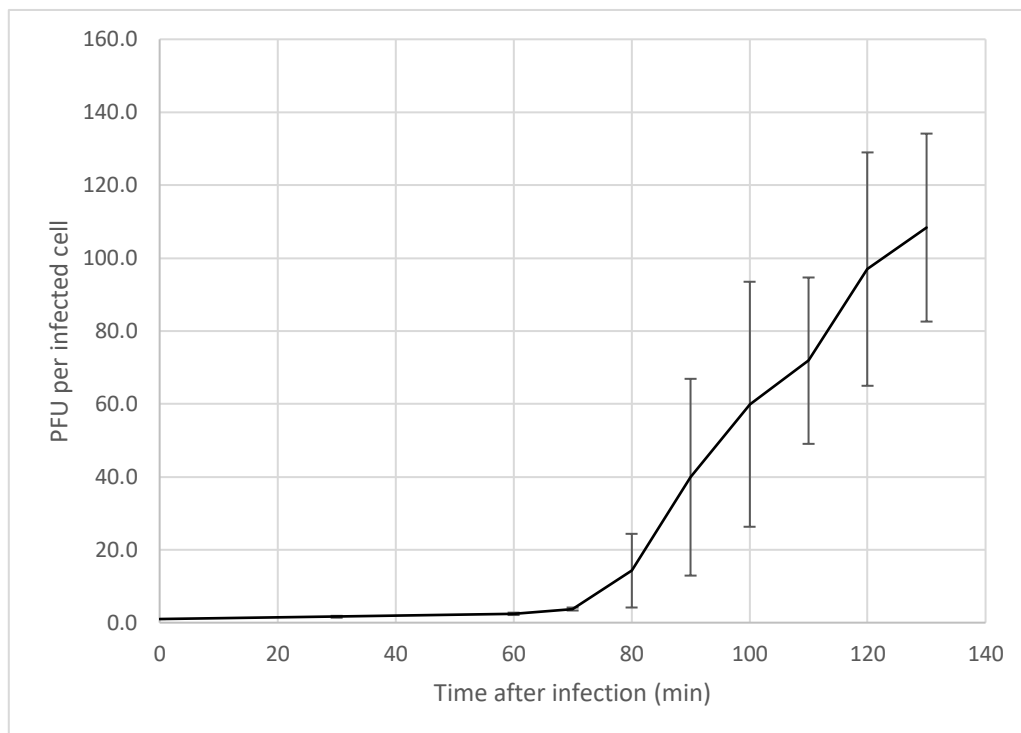


Fig. 3: One-step growth curve of phage fHo-Pae01 in its standard host *P. aeruginosa* #5525 as PFU per infected cell at different timepoints. The data points are averages of four experiments at time points 70 minutes, 90 minutes, and 110 minutes, and of three experiments for the other timepoints. The latent period was 70 minutes. The variation between the experiments did not allow for a reliable estimation of the burst size.

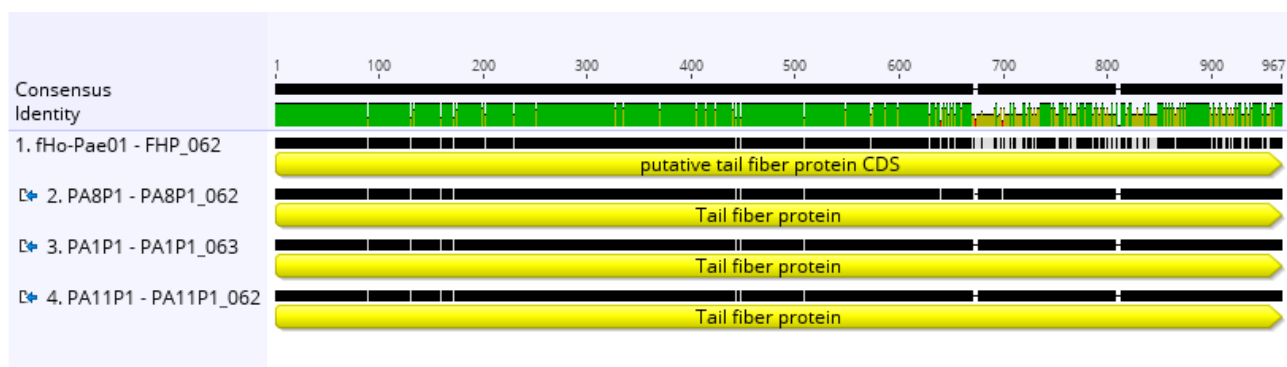


Fig. 4. An alignment of the putative host recognizing tail proteins of fHo-Pae01, PA1P1, PA8P1, and PA11P1. Created with Geneious 11.1.5 (<https://www.geneious.com>) software. The height and color of the identity bar indicates the mean pairwise identity over all pairs in the column (Green: 100% identity, yellow: 30% - 100% identity, red: below 30% identity). PA1P1_063 and PA11P1_062 are 100.00% identical. PA8P1_062 is 97.40% identical to the latter, with mutations spread evenly along the length of the protein. FHP_062 is 84.06% identical to PA8P1_062, and 82.40% identical to PA1P1_063 and PA11P1_062. The differences between FHP_062 and the others are concentrated on the C terminal end of the protein.

Purification of phage fHo-Pae01

The phage fHo-Pae01 was purified for atomic force microscopy using anion-exchange chromatography by determining the conditions for a step-gradient purification with a linear-gradient run (Fig. S2) before performing the step-gradient run (Fig. S3). The isoelectric point of the putative major structural protein, as determined by EMBOSS Pepstats [37] was 5.8560. The pH 8.5 of the buffers was chosen based on the isoelectric point and a previous unsuccessful purification with pH 7.0 (Patinen *et al.* unpublished results).

The amount of phage injected into the column in the step gradient purification, 1.7×10^{11} pfu, was determined by the titer of the lysate as measured before changing the buffer, filtration, or concentration of the sample. The purified phage yield was 5.7×10^9 pfu, and the final yield after changing the buffer was 4.7×10^9 pfu. Thus, the yield of purified phage was approximately 2.8% of the amount that was injected into the column, though a portion of the phages may have been lost during the sample preparation steps before injection.

Imaging

Atomic force microscopy was used to image the fHo-Pae01 virus particle. However, the resolution of the microscope was not optimized for biological samples. Although the objects in the images resemble bacteriophages by shape, no reliable conclusions can be made of them. (Fig. 5)

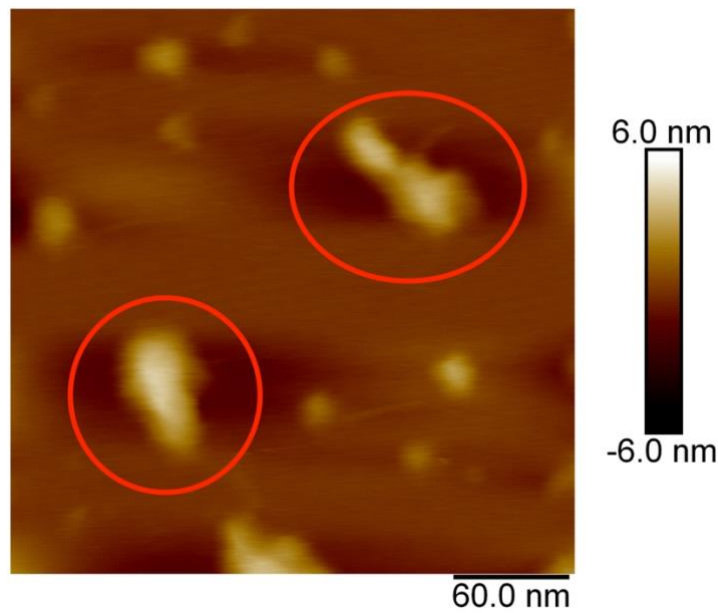


Fig. 5. Image of the purified fHo-Pae01 phage particle taken using atomic force microscopy. Although some particles resembling phages (indicated with red circles) could be found, the resolution of the microscope did not allow any conclusions to be made of the particle.

DISCUSSION

This study reports the fully annotated DNA sequences and infection characteristics of *P. aeruginosa* phages PA1P1, PA8P1 and PA11P1 as well as a new phage fHo-Pae01, isolated in the Skurnik group. All studied phages were predicted to belong to the same species with *Pseudomonas* phages 14_1, JG024, NP3, PII10A, SL1, and SN of the *Pbunavirus* genus, but to a different species than the reference phage PB1. The phages all had genomes of 65 – 67 kbp. The small genome size is characteristic of *Pbunaviruses* unlike in many other members of the *Myoviridae* family [16]. The atomic force microscopy failed to produce further insight on the morphology of fHo-Pae01. This method of imaging phages has previously shown some promising results [40,41], but the atomic force microscope used may not have met the necessary standards for imaging particles on the nanometer scale. The phage has since been imaged by transmission electron microscopy (Pulkkinen *et al.*, manuscript under preparation), but that is beyond the scope of this thesis.

No tRNA-coding genes were identified, which indicates that phages are dependent on the host tRNA molecules and may use codon-optimization to exploit the translation machinery of the host [42]. Additionally, all four phages were concluded to likely be harmless to humans, as no potential virulence-associated, toxic, or antibiotic resistance genes were recognized. Moreover, no genes associated with a temperate infection cycle were identified, so all of the phages are assumed to be

strictly lytic. Still, more than 70% of the annotated genes had unknown functions, which is typical of bacteriophages (NCBI database) and demonstrates how much is still unknown about bacterial viruses. The annotated genomes of PA1P1, PA8P1, and PA11P1 will be submitted to the GenBank database shortly.

The GC content of approximately 56% in the studied phage genomes was similar to many other PB1-like *P. aeruginosa* phages [43]. Often, the phage and host genomes are similar in GC content. However, it is common for *P. aeruginosa* phages to have a significantly lower GC content compared to the bacterial host [44]. No sequencing data of the bacterial hosts used in this study was available, but 186 of the 187 complete *P. aeruginosa* bacterial genomes on the NCBI database had a GC content of 65.08 – 66.84%. Therefore, these phages likely exhibit a similar difference in GC content to their hosts (approximately 10 percentage points lower) as previously reported for other *P. aeruginosa* phages [43].

The G-rich nucleotide sequence observed in all four phage genomes is a common feature of PB1-like phages, as this stretch has been predicted to be a site for ribosomal frameshift [43]. This may also be the case for the four phages studied here. It is possible that the slippery sequence of the repeated G nucleotide enables multiple proteins to be translated from the same mRNA sequence, depending on ribosomal frameshifts. Assuming the G repeat is nine nucleotides long in reality, a +1 frameshift is likely to take place, which would yield a merged form of PA1P1_061A and PA1P1_061B. In this case the same would be true for PA8P1_060A and PA8P1_060B as well as PA11P1_060A and PA11P1_060B.

A +1 shift is known to be common in dsDNA phages and has been well documented in many phages across multiple host organisms [45-47]. If a -1 frameshift took place on this site, a stop codon would form before the origin of the PA1P1_061B (PA8P1_060B, PA11P1_060B) gene. Thus, two proteins originating from the same site may be produced: a short protein with no ribosomal frameshift (PA1P1_061A, PA8P1_060A, PA11P1_060A), and a longer protein caused by a +1 frameshift (PA1P1_061A + PA1P1_061B, PA8P1_060A + PA8P1_060B, PA11P1_060A + PA11P1_060B). It would be interesting to analyze the protein production in an infected cell to find out which frameshift could be observed *in vivo*, and in what ratios the different products of this site are produced. Previous studies would suggest the shorter product with no frameshift to be the major product [46-48].

Of the four phages studied, PA1P1 and PA11P1 are the most promising candidates to be used for phage therapy as their host ranges are the broadest. This is a desirable property, as it indicates a higher probability of the phage being able to infect new host strains. Here, the tail fiber protein

predicted to mediate the adsorption of the phage to the host cell somewhat correlated with the observed host ranges. However, I assume this protein not to be the only factor mediating the phage attachment to its receptor as PA1P1_063 and PA11P1_062 were 100.00% identical, yet their host ranges differed marginally.

Phages are often applied as a cocktail, a mixture of two or more phages infecting the same host, to prevent the development of phage resistance and to improve the efficiency of the treatment [49,50]. For this purpose, phages with the widest host ranges are chosen to produce the broadest lytic range possible for the final cocktail. Therefore, it is exceedingly important for the establishment of efficient phage therapy to discover multiple phages infecting the same host species of bacteria. Phage resistance for therapy products develops when the receptor of the host bacteria is lost or mutated [11], so phages utilizing differing receptors should be prioritized. For that reason, it would be beneficial to determine the receptors of the phages in future studies. Often, phage receptors such as lipopolysaccharides also act as virulence factors. The mutations leading to phage resistance in these structures may even be beneficial, making the pathogen less virulent and more susceptible to the immune system [11].

The one-step growth curve characterizing the infection cycle of fHo-Pae01 revealed the latent period to be 70 minutes long. This result deviates from the 35 – 50 minutes previously reported for most PB1-like phages [35,51,52]. It has been documented that longer latent periods correlate with higher burst sizes at the lysis [53,54]. This is due to the phage having more time to utilize the resources of the host [53]. Thus, it would be reasonable to expect a large burst size in relation to other PB1-like phages. The optimization of the one-step growth curve method will be continued to determine the burst size of fHo-Pae01, although it is beyond the scope of this thesis. I hypothesize that the 15 minute adsorption time used before for *Pseudomonas* phage JG024 [35] was too long to produce a sufficiently synchronized infection for fHo-Pae01.

The optimization of the purification conditions must also be continued. When purifying the fHo-Pae01 phage with anion-exchange chromatography, a significant number of the phages were lost, presumably caused by the weak attachment of the phage to the column. The yield 2.8% was merely a fraction of the >70% achieved for other phages in the Skurnik group. The bond could be tightened by raising the pH of the buffers used, but this would likely denature the phage capsids and render them unviable. For therapeutic use, an alternative approach for purification should be used. Promising results have recently been achieved by combining ultrafiltration with commercial

endotoxin binding columns. This method may even be faster and more efficient in separating bacterial LPS from the phage lysate than many of the other commonly used methods [55].

In conclusion, no indication of genes encoding antibiotic-resistance, toxins or lysogeny-associated was observed, suggesting the four phages – fHo-Pae01, PA1P1, PA8P1, and PA11P1 – to be potentially safe to use in phage therapy to treat *P. aeruginosa* infections and in other possible applications such as biofilm prevention. The wide host ranges of PA1P1 and PA11P1 make them the most compelling candidates for treatment. In the future, clinical studies should be carried out to determine the *in vivo* efficiency of these phages in curing infections.

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Supplementary material

Table S1. *Pseudomonas aeruginosa* strains used in laboratory work.

Table S2. Phages used in the phylogenetic tree.

Table S3. Predicted genes of *P. aeruginosa* phage fHo-Pae01.

Table S4. Predicted genes of *P. aeruginosa* phage PA1P1.

Table S5. Predicted genes of *P. aeruginosa* phage PA8P1.

Table S6. Predicted genes of *P. aeruginosa* phage PA11P1.

Table S7. Detailed results of the host range screening.

Fig. S1. A demonstrative image of the evaluation of the host range screening results.

Fig. S2. Linear gradient purification of phage fHo-Pae01.

Fig. S3. Step-gradient purification of phage fHo-Pae01.

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Table S1: *Pseudomonas aeruginosa* strains used in laboratory work

<i>Pseudomonas aeruginosa</i> strain access number in Skurnik lab	Official name	Notes	Reference/origin
5513			HUSLAB
5514			HUSLAB
5525			HUSLAB
5537			HUSLAB
5538		MDR	HUSLAB
5539		MDR	HUSLAB
5548			HUSLAB
5550			HUSLAB
5551			HUSLAB
5553			HUSLAB
5668			HUSLAB
5669			HUSLAB
5670			HUSLAB
5671			HUSLAB
5672			HUSLAB
5740			HUSLAB
5741			HUSLAB
5742			HUSLAB
5743			HUSLAB
5745			HUSLAB
5746			HUSLAB
5747			HUSLAB
5826			HUSLAB
5827		MDR	HUSLAB
5828			HUSLAB
5829			HUSLAB
5831			HUSLAB
5832			HUSLAB
5833		MDR	HUSLAB
5834		MDR	HUSLAB
5835			HUSLAB
5836			HUSLAB
5837			HUSLAB
5838			HUSLAB
5839			HUSLAB
5840			HUSLAB
5841			HUSLAB
5842		MDR	HUSLAB
5844		MDR	HUSLAB
5845			HUSLAB
5846			HUSLAB
5847			HUSLAB
5848			HUSLAB
6327	PA1		(Mattila, Ruotsalainen & Jalasvuori 2015)
6329	PA8		(Mattila, Ruotsalainen & Jalasvuori 2015)
6331	PA11		(Mattila, Ruotsalainen & Jalasvuori 2015)
6663			HUSLAB

According to the GDPR law, official strain codes must not be presented for clinical strains from HUSLAB to protect patient identity.

MDR: strain confirmed to be multidrug resistant.

Table S2: Phages used in the phylogenetic tree.

Phage name	GenBank accession no.
<i>Pseudomonas</i> phage Kraken	KT372692.1
Pbunaliikevirus phiVader	KT254130.1
<i>Pseudomonas</i> phage Poseidon	KT372696.1
<i>Pseudomonas</i> phage Kula	KT372693.1
<i>Pseudomonas</i> phage Nessie	KT372695.1
<i>Pseudomonas aeruginosa</i> isolate ph_PII10A	LT594786.1
<i>Pseudomonas</i> phage SN	FM887021.1
<i>Pseudomonas</i> phage JG024	GU815091.1
<i>Pseudomonas</i> phage NP3	KU198331.1
<i>Pseudomonas</i> phage 14-1	FM897211.1
<i>Pseudomonas</i> phage vB_Pae_PS44	KM434184.1
<i>Pseudomonas</i> phage vB_PaeM_E215	MF490241.1
<i>Pseudomonas</i> phage NH-4	JN254800.1
<i>Pseudomonas</i> phage SL1	MF768470.1
<i>Pseudomonas</i> phage phiKT28	KP340287.1
<i>Pseudomonas</i> phage KPP12 DNA	AB560486.1
<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27	LN610579.1
<i>Pseudomonas</i> phage vB_PaeM_E217	MF490240.1
<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1	KR869157.1
<i>Pseudomonas</i> phage BrSP1	MF623055.1
<i>Pseudomonas</i> phage S12-1 DNA	LC102730.1
<i>Pseudomonas</i> phage LMA2	FM201282.1

Table S3: Predicted genes of *P. aeruginosa* phage fHo-Pae01. Annotations made by Elsi Pulkkinen. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC (%)	Protein length (aa)	Amino acid sequence identity/similarity to best homologs (% amino acid identity)	E-value (BLAST)	Accession no
FHP001	665 - 1234	59.5	570	hypothetical protein PPSN_gp77 [<i>Pseudomonas</i> phage SN] hypothetical protein [<i>Pseudomonas</i> phage S12-1]	7e-138 1e-137	YP_002418883.1 BAU16489.1
FHP002c	1401 - 2015	56.1	615	hypothetical protein PII10A_02 [<i>Pseudomonas aeruginosa</i>] hypothetical protein PPSN_gp78 [<i>Pseudomonas</i> phage SN]	1e-142 4e-142	SBT96684.1 YP_002418884.1
FHP003c	2207 - 2878	59.2	672	putative minor head protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	4e-157 1e-143	SBT96685.1 YP_007238232.1
FHP004c	2889 - 3200	55.7	312	hypothetical protein PP141_gp79 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeME217_00082 [<i>Pseudomonas</i> phage vB_PaeM_E217]	1e-72 7e-72	YP_002364387.1 ASZ72466.1
FHP005c	3253-3474	51.4	222	hypothetical protein PP141_gp80 [<i>Pseudomonas</i> phage 14-1] hypothetical protein I7A_082c [<i>Pseudomonas</i> phage NH-4]	3e-44 6e-44	YP_002364388.1 YP_007002628.1
FHP006c	3484 - 3738	56.9	255	hypothetical protein PP141_gp81 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas aeruginosa</i>]	2e-53 5e-50	YP_002364389.1 WP_121332560.1

FHP007c	3792 - 4016	55.6	225	hypothetical protein LBL3_gp79 [<i>Pseudomonas</i> phage LBL3] hypothetical protein PPSN_gp83 [<i>Pseudomonas</i> phage SN]	3e-47 2e-46	YP_002154224.1 YP_002418889.1
FHP008c	4082 - 4408	55.7	327	hypothetical protein [Pbunlikevirus phiVader] hypothetical protein [<i>Pseudomonas</i> phage E79]	2e-73 3e-73	ALJ99257.1 AXF41825.1
FHP009c	4405 - 5052	59.1	648	hypothetical protein [<i>Pseudomonas</i> phage PA5] hypothetical protein PJG24_088 [<i>Pseudomonas</i> phage JG024]	9e-149 5e-148	APD20735.1 YP_006200852.1
FHP010c	5084 - 5293	58.1	210	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PA01_Ab27]	7e-45 8e-40	WP_015994944.1 YP_009124313.1
FHP011c	5290 - 5505	51.9	216	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_090 [<i>Pseudomonas</i> phage JG024]	2e-43 1e-42	YP_009215142.1 YP_006200854.1
FHP012c	5502 - 5702	54.2	201	hypothetical protein [<i>Pseudomonas</i> phage NP3] hypothetical protein PP141_gp87 [<i>Pseudomonas</i> phage 14-1]	5e-41 8e-41	AMQ76208.1 YP_002364395.1
FHP013c	5699 - 5950	51.2	252	hypothetical protein LMA2_gp89 [<i>Pseudomonas</i> phage LMA2] hypothetical protein [<i>Pseudomonas</i> phage NP3]	1e-53 2e-53	YP_002154322.1 AMQ76209.1
FHP014c	6037 - 6225	50.3	189	hypothetical protein PP141_gp89 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PII10A_14 [<i>Pseudomonas aeruginosa</i>]	9e-40 1e-37	YP_002364397.1 SBT96696.1
FHP015c	6228 - 7145	54.5	918	tail length tape-measure protein [<i>Pseudomonas</i> phage E79] tail length tape-measure protein [<i>Pseudomonas</i> phage NP3]	0 0	AXF41778.1 AMQ76211.1
FHP016c	7192 - 7494	53.8	303	hypothetical protein PPSN_gp01 [<i>Pseudomonas</i> phage SN] hypothetical protein vBPaeMLS1_39 [<i>Pseudomonas</i> phage vB_PaeM_LS1]	5e-64 4e-60	YP_002418807.1 AVJ48808.1
FHP017c	7822 - 7968	53.1	147	hypothetical protein PPSN_gp03 [<i>Pseudomonas</i> phage SN] hypothetical protein SAMN05216409_118116 [<i>Pseudomonas lutea</i>]	6e-23 6e-13	YP_002418809.1 SER37912.1
FHP018	8144 - 9526	53.1	1383	terminase large subunit [<i>Pseudomonas</i> phage vB_Pae436M-8] putative terminase large subunit [<i>Pseudomonas</i> phage LBL3]	0 0	ANT44190.1 YP_002154147.1
FHP019c	9563 - 9946	59.4	384	hypothetical protein PP141_gp04 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage NP3]	5e-85 1e-84	YP_002364312.1 AMQ76120.1
FHP020c	9943 - 10161	58.0	219	hypothetical protein PPSN_gp06 [<i>Pseudomonas</i> phage SN] hypothetical protein BrSP1_22 [<i>Pseudomonas</i> phage BrSP1]	1e-44 3e-44	YP_002418812.1 ATI16273.1
FHP021c	10161 - 10511	61.8	351	hypothetical protein PPSN_gp07 [<i>Pseudomonas</i> phage SN] hypothetical protein SL1_06 [<i>Pseudomonas</i> phage SL1]	4e-78 1e-75	YP_002418813.1 AUS03281.1
FHP022c	10555 - 10953	59.4	399	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [<i>Pseudomonas</i> phage LBL3]	8e-86 1e-84	YP_009215129.1 YP_002154151.1
FHP023c	10956 - 11735	55.6	780	hypothetical protein PP141_gp08 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vB_Pae_PS44_00009 [<i>Pseudomonas</i> phage vB_Pae_PS44]	0 0	YP_002364316.1 YP_009211333.1
FHP024c	11823 - 12254	61.3	432	hypothetical protein BrSP1_26 [<i>Pseudomonas</i> phage BrSP1] hypothetical protein [<i>Pseudomonas aeruginosa</i>]	3e-82 6e-80	ATI16277.1 WP_121332544.1
FHP025c	12271 - 12858	57.7	588	hypothetical protein [<i>Pseudomonas</i> phage NP3] hypothetical protein PP141_gp10 [<i>Pseudomonas</i> phage 14-1]	2e-143 1e-142	AMQ76126.1 YP_002364318.1
FHP026c	12868 - 12963	52.1	96	hypothetical protein vBPaeME215_00084 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein vB_Pae_PS44_00012 [<i>Pseudomonas</i> phage vB_Pae_PS44]	4e-11 1e-10	ASZ72562.1 YP_009211336.1
FHP027c	12960 - 13892	56.8	933	hypothetical protein vBPaeME215_00085 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein PP141_gp12 [<i>Pseudomonas</i> phage 14-1]	0 0	ASZ72563.1 YP_002364320.1

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FHP028c	13996 - 14496	57.1	501	hypothetical protein vBPaeME215_00086 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein PPSN_gp14 [<i>Pseudomonas</i> phage SN]	4e-120 1e-119	ASZ72564.1 YP_002418820.1
FHP029	14519 - 14686	49.4	168	ERROR: "No significant similarity found"		
FHP030c	14987 - 15298	52.6	312	hypothetical protein PII10A_31 [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	3e-68 3e-67	SBT96713.1 YP_009124336.1
FHP031c	15304 - 15516	58.2	213	hypothetical protein [Burkholderia vietnamiensis] hypothetical protein vB_Pae_PS44_00018 [<i>Pseudomonas</i> phage vB_Pae_PS44]	4e-41 2e-40	WP_016057510.1 YP_009211342.1
FHP032c	15504 - 15827	56.5	324	hypothetical protein LMA2_gp15 [<i>Pseudomonas</i> phage LMA2] hypothetical protein vB_Pae_PS44_00019 [<i>Pseudomonas</i> phage vB_Pae_PS44]	3e-75 2e-73	YP_002154249.1 YP_009211343.1
FHP033c	15859 - 16260	53.0	402	hypothetical protein LMA2_gp16 [<i>Pseudomonas</i> phage LMA2] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	2e-92 9e-92	YP_002154250.1 YP_009124339.1
FHP034	16441 - 18738	56.9	2298	putative portal protein [<i>Pseudomonas aeruginosa</i>] putative minor head protein [<i>Pseudomonas</i> phage PB1]	0 0	SBT96717.1 YP_002455948.1
FHP035	18738 - 19574	53.6	837	putative minor head protein [<i>Pseudomonas</i> phage KPP12] putative head protein [<i>Pseudomonas</i> phage PB1]	0 0	YP_007238173.1 YP_002455949.1
FHP036	19593 - 19799	55.6	207	hypothetical protein PPSN_gp21 [<i>Pseudomonas</i> phage SN] hypothetical protein LBL3_gp17 [<i>Pseudomonas</i> phage LBL3]	2e-41 6e-40	YP_002418827.1 YP_002154162.1
FHP037	19796 - 19936	53.2	141	hypothetical protein PPSN_gp22 [<i>Pseudomonas</i> phage SN] hypothetical protein PJG24_021 [<i>Pseudomonas</i> phage JG024]	4e-23 4e-22	YP_002418828.1 YP_006200786.1
FHP038	19936 - 20061	42.9	126	No significant similarity found.		
FHP039	20489 - 21871	58.2	1383	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PP141_gp22 [<i>Pseudomonas</i> phage 14-1]	0 0	YP_009215206.1 YP_002364330.1
FHP040	21875 - 22510	62.6	636	hypothetical protein PP141_gp23 [<i>Pseudomonas</i> phage 14-1] structural protein [<i>Pseudomonas</i> phage SN]	5e-148 2e-147	YP_002364331.1 YP_002418830.1
FHP041	22520 - 23668	61.0	1149	hypothetical protein PP141_gp24 [<i>Pseudomonas</i> phage 14-1] putative major structural protein [<i>Pseudomonas</i> phage LMA2]	0 0	YP_002364332.1 YP_002154257.1
FHP042	23770 - 24207	55.3	438	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	6e-104 2e-103	WP_121332534.1 YP_007238179.1
FHP043	24222 - 24689	59.4	468	DUF4054 domain-containing protein [<i>Pseudomonas aeruginosa</i>] putative structural protein [<i>Pseudomonas</i> phage LMA2]	5e-110 2e-108	WP_016066139.1 YP_002154259.1
FHP044	24686 - 25084	52.1	399	putative structural protein [<i>Pseudomonas</i> phage KPP12] structural protein [<i>Pseudomonas</i> phage phiKTN6]	4e-92 1e-91	YP_007238181.1 AKJ71558.1
FHP045	25092 - 25643	48.2	552	hypothetical protein vBPaeME215_00007 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	1e-133 2e-133	ASZ72485.1 YP_009124349.1
FHP046	25640 - 26221	54.8	582	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	3e-137 1e-136	WP_015981230.1 YP_007238183.1
FHP047	26237 - 27751	59.8	1515	hypothetical protein vB_Pae436M-8_30 [<i>Pseudomonas</i> phage vB_Pae436M-8] putative structural protein [<i>Pseudomonas</i> phage LMA2]	0 0	ANT44216.1 YP_002154263.1
FHP048	27810 - 28262	59.2	453	hypothetical protein [<i>Pseudomonas aeruginosa</i>] structural protein [<i>Pseudomonas</i> phage phiKT28]	2e-103 2e-102	WP_015992745.1 AKJ71471.1
FHP049	28262 - 28585	54.3	324	hypothetical protein [<i>Pseudomonas aeruginosa</i>] putative structural protein [<i>Pseudomonas</i> phage JG024]	2e-75 6e-75	WP_015992746.1 YP_006200797.1

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FHP050	28582 - 28932	52.4	351	hypothetical protein [<i>Pseudomonas aeruginosa</i>] structural protein [<i>Pseudomonas</i> phage SL1]	3e-78 1e-77	WP_015992747.1 AUS03345.1
FHP051	28934 - 29365	63.9	432	hypothetical protein LMA2_gp33 [<i>Pseudomonas</i> phage LMA2] hypothetical protein vBPaeMDP1_0034 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	6e-94 4e-93	YP_002154267.1 AKP24421.1
FHP052	29375 - 29878	51.6	504	hypothetical protein [<i>Pseudomonas aeruginosa</i>] structural protein [<i>Pseudomonas</i> phage SN]	3e-114 6e-114	WP_015992749.1 YP_002418842.1
FHP053	29878 - 30417	51.1	540	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative structural protein [<i>Pseudomonas</i> phage LBL3]	6e-128 2e-127	YP_002154269.1 YP_002154178.1
FHP054	30426 - 31019	47.3	594	putative structural protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein vBPaeME217_00038 [<i>Pseudomonas</i> phage vB_PaeM_E217]	4e-138 2e-137	YP_007238190.1 ASZ72422.1
FHP055	31029 - 31457	56.6	429	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein LMA2_gp37 [<i>Pseudomonas</i> phage LMA2]	5e-101 2e-100	WP_121332529.1 YP_002154271.1
FHP056	31461 - 34037	58.1	2577	putative lytic tail protein [<i>Pseudomonas</i> phage LMA2] internal (core) protein [<i>Pseudomonas</i> phage NP3]	0 0	YP_002154272.1 AMQ76156.1
FHP057	34037 - 34900	51.9	864	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative structural protein [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	0 0	YP_002154273.1 AKP24427.1
FHP058	34900 - 35433	48.1	534	hypothetical protein PP141_gp41 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	2e-127 6e-127	YP_002364349.1 YP_009215187.1
FHP059	35828 - 36154	53.2	327	putative baseplate protein [<i>Pseudomonas</i> phage JG024] baseplate protein [<i>Pseudomonas</i> phage phiKTN6]	1e-71 1e-71	YP_006200807.1 AKJ71573.1
FHP060	36211 - 37464	57.7	1254	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative baseplate protein [<i>Pseudomonas</i> phage SN]	0 0	YP_002154276.1 YP_002418850.1
FHP061	37461 - 38975	56.0	1515	hypothetical protein PP141_gp44 [<i>Pseudomonas</i> phage 14-1] structural protein [<i>Pseudomonas</i> phage vB_Pae436M-8]	0 0	YP_002364352.1 ANT44230.1
FHP062	38980 - 41874	57.1	2895	hypothetical protein vBPaeME215_00024 [<i>Pseudomonas</i> phage vB_PaeM_E215] putative tail fiber protein [<i>Pseudomonas aeruginosa</i>]	0 0	ASZ72502.1 SBT96745.1
FHP063	41876 - 42304	58.5	429	tail fibers component [<i>Pseudomonas</i> phage phiKTN6] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	3e-99 3e-99	AKJ71577.1 YP_009124367.1
FHP064	42304 - 42966	60	663	putative lytic enzyme [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27] endolysin [<i>Pseudomonas</i> phage PB1]	3e-162 9e-161	YP_009124368.1 YP_002455978.1
FHP065c	42990 - 43241	51.2	252	hypothetical protein PP141_gp48 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [<i>Pseudomonas</i> phage LMA2]	2e-50 3e-50	YP_002364356.1 YP_002154281.1
FHP066c	43521 - 44432	57.2	912	putative DNA ligase [<i>Pseudomonas aeruginosa</i>] hypothetical protein PP141_gp49 [<i>Pseudomonas</i> phage 14-1]	0 0	SBT96752.1 YP_002364357.1
FHP067c	44487 - 45041	53.7	555	hypothetical protein I7A_051c [<i>Pseudomonas</i> phage NH-4] hypothetical protein [<i>Pseudomonas</i> phage KPP22]	2e-133 5e-133	YP_007002597.1 BAU20664.1
FHP068c	45038 - 45646	60.6	609	hypothetical protein vBPaeME215_00030 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein ORF050 [<i>Pseudomonas</i> phage F8]	9e-139 1e-136	ASZ72508.1 YP_001294467.1
FHP069c	45700 - 46599	60.1	900	hypothetical protein PP141_gp52 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	0 0	YP_002364360.1 YP_009215176.1
FHP070c	46688 - 47308	53.9	621	hypothetical protein LMA2_gp52 [<i>Pseudomonas</i> phage LMA2] hypothetical protein I7A_054c [<i>Pseudomonas</i> phage NH-4]	3e-145 3e-145	YP_002154286.1 YP_007002600.1

FHP071c	47403 - 48962	54.6	1560	DNA helicase [<i>Pseudomonas</i> phage DL68] hypothetical protein PP141_gp54 [<i>Pseudomonas</i> phage 14-1]	0 0	YP_009215174.1 YP_002364362.1
FHP072c	48959 - 49369	55.7	411	hypothetical protein [<i>Pseudomonas</i> phage KPP12] putative DNA helicase [<i>Pseudomonas</i> phage NH-4]	2e-94 3e-94	YP_007238208.1 YP_007002602.1
FHP073c	49362 - 52469	55.2	3108	DNA polymerase III alpha subunit [<i>Pseudomonas</i> phage vB_PaeM_LS1] putative DNA polymerase [<i>Pseudomonas</i> phage KPP12]	0 0	AVJ48844.1 YP_007238209.1
FHP074c	52469 - 53023	53.0	555	putative DNA polymerase III epsilon subunit [<i>Pseudomonas</i> phage NH-4] putative DNA polymerase III epsilon subunit [<i>Pseudomonas</i> phage LMA2]	2e-135 3e-135	YP_007002604.1 YP_002154290.1
FHP075c	53099 - 54115	58.4	1017	hypothetical protein PP141_gp58 [<i>Pseudomonas</i> phage 14-1] putative 3'-phosphatase 5'-polynucleotide kinase [<i>Pseudomonas aeruginosa</i>]	0 0	YP_002364366.1 SBT96767.1
FHP076c	54118 - 54309	47.4	192	hypothetical protein phiKT28_061 [<i>Pseudomonas</i> phage phiKT28] hypothetical protein PJG24_060 [<i>Pseudomonas</i> phage JG024]	1e-35 3e-35	AKJ71499.1 YP_006200824.1
FHP077c	54311 - 55228	58.0	918	putative thymidylate synthase [<i>Pseudomonas</i> phage KPP12] putative thymidylate synthase [<i>Pseudomonas</i> phage JG024]	0 0	YP_007238213.1 YP_006200825.1
FHP078c	55228 - 55434	51.7	207	hypothetical protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein [<i>Pseudomonas</i> phage PA5]	7e-40 1e-39	YP_007238214.1 APD20762.1
FHP079c	55442 - 55672	56.7	231	hypothetical protein PPSN_gp63 [<i>Pseudomonas</i> phage SN] hypothetical protein PP141_gp62 [<i>Pseudomonas</i> phage 14-1]	5e-49 1e-48	YP_002418869.1 YP_002364370.1
FHP080c	55705 - 55923	53.9	219	hypothetical protein LMA2_gp62 [<i>Pseudomonas</i> phage LMA2] tail assembly protein [<i>Pseudomonas</i> phage phiKTN6]	2e-46 9e-46	YP_002154296.1 AKJ71594.1
FHP081c	55907 - 56125	58.0	219	hypothetical protein phiKTN6_063 [<i>Pseudomonas</i> phage phiKTN6] hypothetical protein I7A_065c [<i>Pseudomonas</i> phage NH-4]	1e-43 1e-43	AKJ71595.1 YP_007002611.1
FHP082c	56125 - 56355	58.9	231	hypothetical protein PP141_gp65 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp62 [<i>Pseudomonas</i> phage LBL3]	6e-50 1e-49	YP_002364373.1 YP_002154207.1
FHP083c	56443 - 57444	55.3	1002	hypothetical protein PP141_gp66 [<i>Pseudomonas</i> phage 14-1] hypothetical protein ORF065 [<i>Pseudomonas</i> phage F8]	0 0	YP_002364374.1 YP_001294482.1
FHP084c	57552 - 58370	62.0	819	hypothetical protein [<i>Pseudomonas</i> phage NP3] hypothetical protein PP141_gp67 [<i>Pseudomonas</i> phage 14-1]	4e-177 2e-102	AMQ76185.1 YP_002364375.1
FHP085c	58532 - 59719	55.1	1188	putative ATP-dependent exonuclease V [<i>Pseudomonas</i> phage SN] ATP-dependent exonuclease [<i>Pseudomonas</i> phage PB1]	0 0	YP_002418875.1 YP_002456000.1
FHP086c	59706 - 60128	56.7	423	hypothetical protein PP141_gp69 [<i>Pseudomonas</i> phage 14-1] hypothetical protein ORF068 [<i>Pseudomonas</i> phage F8]	4e-98 2e-97	YP_002364377.1 YP_001294485.1
FHP087	60297 - 61118	58.6	822	hypothetical protein PJG24_071 [<i>Pseudomonas</i> phage JG024] hypothetical protein PP141_gp70 [<i>Pseudomonas</i> phage 14-1]	0 0	YP_006200835.1 YP_002364378.1
FHP088	61129 - 62433	58.5	1305	hypothetical protein PP141_gp71 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp68 [<i>Pseudomonas</i> phage LBL3]	0 0	YP_002364379.1 YP_002154213.1
FHP089	62457 - 62906	58.0	450	hypothetical protein PP141_gp72 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage NP3]	4e-106 6e-106	YP_002364380.1 AMQ76190.1
FHP090	62903 - 63979	57.5	1077	hypothetical protein PP141_gp73 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeMLS1_59 [<i>Pseudomonas</i> phage vB_PaeM_LS1]	0 0	YP_002364381.1 AVJ48828.1

FHP091	63985 - 64134	50	150	hypothetical protein ORF073 [<i>Pseudomonas</i> phage F8] hypothetical protein phiKTN6_073 [<i>Pseudomonas</i> phage phiKTN6]	3e-10 3e-10	YP_001294490.1 AKJ71605.1
FHP092	64317 - 66056	54.0	1740	putative DNA primase [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1] DNA primase [<i>Pseudomonas</i> phage vB_Pae436M-8]	0 0	AKP24459.1 ANT44262.1

Table S4: Predicted genes of *P. aeruginosa* phage PA1P1. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC (%)	Protein lenght (aa)	Amino acid sequence identity/similarity to best homologs (% amino acid identity)	E-value (BLAST)	Accession no.
PA1P1_001	604 - 1185	58.2	193	hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27] hypothetical protein LMA2_gp76 [<i>Pseudomonas</i> phage LMA2]	4E-137 3E-136	YP_009124304.1 YP_002154309.1
PA1P1_002c	1953 - 1342	55.1	203	hypothetical protein PP141_gp77 [<i>Pseudomonas</i> phage 14-1] hypothetical protein SL1_26 [<i>Pseudomonas</i> phage SL1]	5E-144 3E-143	YP_002364385.1 AUS03301.1
PA1P1_003c	2829 - 2143	60.0	228	hypothetical protein PP141_gp78 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeME215_00057 [<i>Pseudomonas</i> phage vB_PaeM_E215]	3E-157 1E-156	YP_002364386.1 ASZ72535.1
PA1P1_004c	3151 - 2840	55.8	103	hypothetical protein vBPaeMDP1_0076 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1] hypothetical protein BrSP1_5 [<i>Pseudomonas</i> phage BrSP1]	1E-71 4E-71	AKP24463.1 ATI16257.1
PA1P1_005c	3425 - 3204	52.7	73	hypothetical protein PP141_gp80 [<i>Pseudomonas</i> phage 14-1] hypothetical protein I7A_082c [<i>Pseudomonas</i> phage NH-4]	3E-44 5E-44	YP_002364388.1 YP_007002628.1
PA1P1_006c	3689 - 3435	56.9	84	hypothetical protein PP141_gp81 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage KPP22]	2E-53 5E-49	YP_002364389.1 BAU20633.1
PA1P1_007c	3967 - 3743	55.6	74	hypothetical protein LBL3_gp79 [<i>Pseudomonas</i> phage LBL3] hypothetical protein PPSN_gp83 [<i>Pseudomonas</i> phage SN]	3E-47 2E-46	YP_002154224.1 YP_002418889.1
PA1P1_008c	4359 - 4033	55.4	108	hypothetical protein [Pbunlikevirus phiVader] hypothetical protein [<i>Pseudomonas</i> phage E79]	2E-73 2E-73	ALJ99257.1 AXF41825.1
PA1P1_009c	5003 - 4356	59.7	215	hypothetical protein LBL3_gp81 [<i>Pseudomonas</i> phage LBL3] hypothetical protein vB_Pae_PS44_00086 [<i>Pseudomonas</i> phage vB_Pae_PS44]	1E-154 2E-152	YP_002154226.1 YP_009211410.1
PA1P1_010c	5247 - 5035	56.3	70	hypothetical protein phiKTN6_084 [<i>Pseudomonas</i> phage phiKTN6] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	2E-45 4E-44	AKJ71616.1 YP_007238238.1
PA1P1_011c	5432 - 5244	49.2	62	hypothetical protein LBL3_gp83 [<i>Pseudomonas</i> phage LBL3] hypothetical protein LMA2_gp86 [<i>Pseudomonas</i> phage LMA2]	4E-38 4E-35	YP_002154228.1 YP_002154319.1
PA1P1_012c	5644 - 5429	53.7	71	hypothetical protein LBL3_gp84 [<i>Pseudomonas</i> phage LBL3] hypothetical protein PB1_gp89 [<i>Pseudomonas</i> phage PB1]	1E-43 2E-43	YP_002154229.1 YP_002456018.1
PA1P1_013c	5841 - 5641	54.2	66	hypothetical protein PPSN_gp89 [<i>Pseudomonas</i> phage SN] hypothetical protein [<i>Pseudomonas</i> phage NP3]	4E-41 3E-40	YP_002418895.1 AMQ76208.1
PA1P1_014c	6089 - 5838	52.0	83	hypothetical protein PJG24_092 [<i>Pseudomonas</i> phage JG024] hypothetical protein PII10A_13 [<i>Pseudomonas aeruginosa</i>]	2E-53 1E-52	YP_006200856.1 SBT96695.1
PA1P1_015c	6364 - 6176	49.7	62	hypothetical protein PP141_gp89 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PII10A_14 [<i>Pseudomonas aeruginosa</i>]	3E-39 5E-37	YP_002364397.1 SBT96696.1
PA1P1_016c	7284 - 6367	54.6	305	tail length tape-measure protein [<i>Pseudomonas</i> phage NP3] tail length tape-measure protein [<i>Pseudomonas</i> phage E79]	0 0	AMQ76211.1 AXF41778.1
PA1P1_017c	7633 - 7331	53.1	100	hypothetical protein PPSN_gp01 [<i>Pseudomonas</i> phage SN]	1E-63 8E-61	YP_002418807.1 AVJ48808.1

				hypothetical protein vBPaeMLS1_39 [<i>Pseudomonas</i> phage vB_PaeM_LS1]		
PA1P1_018c	7862 - 7689	54.0	57	hypothetical protein PPSN_gp02 [<i>Pseudomonas</i> phage SN] hypothetical protein PII10A_17 [<i>Pseudomonas aeruginosa</i>]	9E-35 2E-34	YP_002418808.1 SBT96699.1
PA1P1_019c	8059 - 7913	53.1	48	hypothetical protein PPSN_gp03 [<i>Pseudomonas</i> phage SN] hypothetical protein SAMN05216409_118116 [<i>Pseudomonas lutea</i>]	5E-23 6E-13	YP_002418809.1 SER37912.1
PA1P1_020	8236 - 9618	52.4	460	putative terminase, large subunit [<i>Pseudomonas aeruginosa</i>] terminase large subunit [<i>Pseudomonas</i> phage E79]	0 0	SBT96701.1 AXF41768.1
PA1P1_021c	10038 - 9655	59.1	127	hypothetical protein PP141_gp04 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage NP3]	3E-86 7E-86	YP_002364312.1 AMQ76120.1
PA1P1_022c	10253 - 10035	54.8	72	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage NP3]	4E-46 3E-45	WP_015994883.1 AMQ76121.1
PA1P1_023c	10603 - 10253	61.3	116	hypothetical protein LBL3_gp05 [<i>Pseudomonas</i> phage LBL3] hypothetical protein SL1_06 [<i>Pseudomonas</i> phage SL1]	4E-78 8E-76	YP_002154150.1 AUS03281.1
PA1P1_024c	11050 - 10649	59.5	133	hypothetical protein PP141_gp07 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PJG24_008 [<i>Pseudomonas</i> phage JG024]	2E-89 1E-88	YP_002364315.1 YP_006200773.1
PA1P1_025c	11832 - 11053	56.9	259	hypothetical protein PP141_gp08 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	0 0	YP_002364316.1 YP_009215128.1
PA1P1_026c	12356 - 11919	61.4	145	hypothetical protein PJG24_010 [<i>Pseudomonas</i> phage JG024] hypothetical protein [<i>Pseudomonas</i> phage DL68]	4E-98 7E-98	YP_006200775.1 YP_009215127.1
PA1P1_027c	12960 - 12373	58.3	195	hypothetical protein [<i>Pseudomonas</i> phage NP3] hypothetical protein PP141_gp10 [<i>Pseudomonas</i> phage 14-1]	4E-144 2E-143	AMQ76126.1 YP_002364318.1
PA1P1_028c	13065 - 12970	49.0	31	hypothetical protein [<i>Pseudomonas</i> phage NP3] hypothetical protein PP141_gp10 [<i>Pseudomonas</i> phage 14-1]	9E-138 5E-137	AMQ76126.1 YP_002364318.1
PA1P1_029c	13994 - 13062	57.2	310	hypothetical protein vB_Pae_PS44_00013 [<i>Pseudomonas</i> phage vB_Pae_PS44] hypothetical protein PPSN_gp13 [<i>Pseudomonas</i> phage SN]	0 0	YP_009211337.1 YP_002418819.1
PA1P1_030c	14597 - 14097	55.7	166	hypothetical protein PP141_gp13 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PJG24_013 [<i>Pseudomonas</i> phage JG024]	4E-120 2E-119	YP_002364321.1 YP_006200778.1
PA1P1_031c	14964 - 14617	53.4	115	hypothetical protein PP141_gp14 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	5E-77 7E-77	YP_002364322.1 YP_009215123.1
PA1P1_032c	15524 - 15213	51.3	103	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_015 [<i>Pseudomonas</i> phage JG024]	2E-68 2E-67	YP_009215122.1 YP_006200780.1
PA1P1_033c	15733 - 15530	58.3	67	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein phiKT28_017 [<i>Pseudomonas</i> phage phiKT28]	3E-41 1E-40	YP_009215121.1 AKJ71455.1
PA1P1_034c	16053 - 15730	55.6	107	hypothetical protein PP141_gp16 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PJG24_016 [<i>Pseudomonas</i> phage JG024]	1E-74 6E-73	YP_002364324.1 YP_006200781.1
PA1P1_035c	16485 - 16084	53.7	133	hypothetical protein PP141_gp17 [<i>Pseudomonas</i> phage 14-1] hypothetical protein phiKT28_019 [<i>Pseudomonas</i> phage phiKT28]	2E-92 9E-92	YP_002364325.1 AKJ71457.1
PA1P1_036	16665 - 18962	56.9	729	hypothetical protein [<i>Pseudomonas</i> phage DL68] minor head-like protein [<i>Pseudomonas</i> phage 14-1]	0 0	YP_009215210.1 YP_002364326.1
PA1P1_037	18962 - 19798	53.4	278	putative minor head protein [<i>Pseudomonas</i> phage SN] putative minor head protein [<i>Pseudomonas</i> phage SL1]	0 0	YP_002418826.1 AUS03359.1
PA1P1_038	19817 - 20023	55.6	68	hypothetical protein PPSN_gp21 [<i>Pseudomonas</i> phage SN] hypothetical protein LBL3_gp17 [<i>Pseudomonas</i> phage LBL3]	2E-41 6E-40	YP_002418827.1 YP_002154162.1
PA1P1_039	20020 - 20160	53.2	46	hypothetical protein PPSN_gp22 [<i>Pseudomonas</i> phage SN]	4E-23 3E-22	YP_002418828.1 YP_006200786.1

				hypothetical protein PJG24_021 [<i>Pseudomonas</i> phage JG024]		
PA1P1_040	20714 - 22108	58.3	464	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PP141_gp22 [<i>Pseudomonas</i> phage 14-1]	0 0	YP_009215206.1 YP_002364330.1
PA1P1_041	22112 - 22747	62.6	211	hypothetical protein PP141_gp23 [<i>Pseudomonas</i> phage 14-1] structural protein [<i>Pseudomonas</i> phage SN]	5E-148 1E-147	YP_002364331.1 YP_002418830.1
PA1P1_042	22757 - 23905	61.0	382	putative major structural protein [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1] hypothetical protein PP141_gp24 [<i>Pseudomonas</i> phage 14-1]	0 0	AKP24411.1 YP_002364332.1
PA1P1_043	24007 - 24444	55.0	145	hypothetical protein vBPaeMDP1_0025 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	6E-104 2E-103	AKP24412.1 YP_007238179.1
PA1P1_044	24459 - 24926	59.2	155	putative structural protein [<i>Pseudomonas</i> phage KPP12] structural protein [<i>Pseudomonas</i> phage phiKTN6]	4E-110 1E-109	YP_007238180.1 AKJ71557.1
PA1P1_045	24923 - 25321	52.1	132	putative structural protein [<i>Pseudomonas</i> phage KPP12] structural protein [<i>Pseudomonas</i> phage phiKTN6]	2E-91 6E-91	YP_007238181.1 AKJ71558.1
PA1P1_046	25329 - 25880	48.4	183	hypothetical protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein vB_Pae_PS44_00031 [<i>Pseudomonas</i> phage vB_Pae_PS44]	3E-133 5E-133	YP_007238182.1 YP_009211355.1
PA1P1_047	25877 - 26458	54.8	193	hypothetical protein ORF028 [<i>Pseudomonas</i> phage F8] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	3E-137 1E-136	YP_001294445.1 YP_007238183.1
PA1P1_048	26474 - 27988	59.1	504	hypothetical protein I7A_031 [<i>Pseudomonas</i> phage NH-4] hypothetical protein vBPaeMDP1_0030 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	0 0	YP_007002577.1 AKP24417.1
PA1P1_049	28047 - 28499	59.6	150	putative structural protein [<i>Pseudomonas</i> phage LMA2] structural protein [<i>Pseudomonas</i> phage phiKTN6]	2E-103 2E-102	YP_002154264.1 AKJ71471.1
PA1P1_050	28499 - 28822	54.6	107	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative structural protein [<i>Pseudomonas</i> phage JG024]	2E-75 5E-75	YP_002154265.1 YP_006200797.1
PA1P1_051	28819 - 29169	53.0	116	putative structural protein [<i>Pseudomonas</i> phage LMA2] structural protein [<i>Pseudomonas</i> phage SL1]	3E-78 1E-77	YP_002154266.1 AUS03345.1
PA1P1_052	29171 - 29602	64.1	143	hypothetical protein PPSN_gp35 [<i>Pseudomonas</i> phage SN] hypothetical protein PII10A_51 [<i>Pseudomonas aeruginosa</i>]	8E-93 2E-92	YP_002418841.1 SBT96733.1
PA1P1_053	29612 - 30115	52.2	167	structural protein [<i>Pseudomonas</i> phage SN] putative structural protein [<i>Pseudomonas</i> phage LMA2]	3E-115 1E-114	YP_002418842.1 YP_002154268.1
PA1P1_054	30115 - 30654	51.1	179	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative structural protein [<i>Pseudomonas</i> phage LBL3]	5E-128 2E-127	YP_002154269.1 YP_002154178.1
PA1P1_055	30663 - 31256	46.8	197	putative structural protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein vBPaeME217_00038 [<i>Pseudomonas</i> phage vB_PaeM_E217]	3E-140 2E-139	YP_007238190.1 ASZ72422.1
PA1P1_056	31266 - 31694	57.1	142	hypothetical protein LBL3_gp35 [<i>Pseudomonas</i> phage LBL3] hypothetical protein phiKTN6_037 [<i>Pseudomonas</i> phage phiKTN6]	4E-101 2E-100	YP_002154180.1 AKJ71569.1
PA1P1_057	31698 - 34274	58.2	858	putative lytic tail protein [<i>Pseudomonas</i> phage LMA2] internal (core) protein [<i>Pseudomonas</i> phage NP3]	0 0	YP_002154272.1 AMQ76156.1
PA1P1_058	34274 - 35137	52.1	287	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative structural protein [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	0 0	YP_002154273.1 AKP24427.1
PA1P1_059	35137 - 35670	48.3	177	hypothetical protein PP141_gp41 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	2E-127 5E-127	YP_002364349.1 YP_009215187.1
PA1P1_060	35726 - 36391	53.0	221	hypothetical protein LMA2_gp41 [<i>Pseudomonas</i> phage LMA2] putative baseplate [<i>Pseudomonas</i> phage KPP12]	2E-160 4E-160	YP_002154275.1 YP_007238195.1

PA1P1_061A	36402 - 36455	42.6	17	hypothetical protein PB1_gp43 [<i>Pseudomonas</i> phage PB1] putative baseplate protein [<i>Pseudomonas</i> phage SN]	3E-09 2E-04	YP_002455973.1 YP_002418850.1
PA1P1_061B	36448 - 37701	57.9	417	hypothetical protein BrSP1_62 [<i>Pseudomonas</i> phage BrSP1] putative baseplate protein [<i>Pseudomonas</i> phage NH-4]	0 0	AT116244.1 YP_007002590.1
PA1P1_062	37698 - 39212	55.7	504	hypothetical protein I7A_045 [<i>Pseudomonas</i> phage NH-4] putative structural protein [<i>Pseudomonas</i> phage JG024]	0 0	YP_007002591.1 YP_006200809.1
PA1P1_063	39217 - 42105	57.8	962	tail fibers protein [<i>Pseudomonas</i> phage NP3] putative tail fiber component [<i>Pseudomonas</i> phage NH-4]	0 0	AMQ76163.1 YP_007002592.1
PA1P1_064	42107 - 42535	58.3	142	hypothetical protein [<i>Pseudomonas</i> phage NP3] putative tail fiber component [<i>Pseudomonas</i> phage JG024]	4E-98 7E-97	AMQ76164.1 YP_006200811.1
PA1P1_065	42535 - 43197	60.5	220	lytic enzyme [<i>Pseudomonas</i> phage NP3] putative endolysin [<i>Pseudomonas</i> phage JG024]	2E-161 7E-161	AMQ76165.1 YP_006200812.1
PA1P1_066c	43472 - 43221	51.2	83	hypothetical protein PP141_gp48 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [<i>Pseudomonas</i> phage LMA2]	2E-50 3E-50	YP_002364356.1 YP_002154281.1
PA1P1_067c	44663 - 43752	56.6	303	DNA ligase [<i>Pseudomonas</i> phage phiKT28] putative DNA ligase [<i>Pseudomonas</i> phage JG024]	0 0	AKJ71489.1 YP_006200814.1
PA1P1_068c	45272 - 44718	54.8	184	DNA binding protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_051 [<i>Pseudomonas</i> phage JG024]	1E-131 9E-131	YP_009215178.1 YP_006200815.1
PA1P1_069c	45874 - 45269	59.6	201	hypothetical protein ORF050 [<i>Pseudomonas</i> phage F8] hypothetical protein PP141_gp51 [<i>Pseudomonas</i> phage 14-1]	3E-137 6E-137	YP_001294467.1 YP_002364359.1
PA1P1_070c	46827 - 45928	59.3	299	hypothetical protein PP141_gp52 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	0 0	YP_002364360.1 YP_009215176.1
PA1P1_071c	47536 - 46916	53.6	206	hypothetical protein vBPaeMLS1_79 [<i>Pseudomonas</i> phage vB_PaeM_LS1] hypothetical protein SL1_50 [<i>Pseudomonas</i> phage SL1]	3E-145 1E-144	AVJ48847.1 AUS03325.1
PA1P1_072c	49190 - 47631	55.2	519	putative helicase [<i>Pseudomonas</i> phage KPP12] putative DNA helicase [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	0 0	YP_007238207.1 AKP24441.1
PA1P1_073c	49597 - 49187	55.2	136	hypothetical protein [<i>Pseudomonas</i> phage KPP12] putative DNA helicase [<i>Pseudomonas</i> phage NH-4]	2E-94 2E-94	YP_007238208.1 YP_007002602.1
PA1P1_074c	52697 - 49590	55.0	1035	putative DNA polymerase [<i>Pseudomonas</i> phage KPP12] DNA polymerase III alpha subunit [<i>Pseudomonas</i> phage vB_PaeM_LS1]	0 0	YP_007238209.1 AVJ48844.1
PA1P1_075c	53251 - 52697	53.3	184	putative DNA polymerase III epsilon subunit [<i>Pseudomonas</i> phage NH-4] putative DNA polymerase III, epsilon subunit [<i>Pseudomonas</i> phage LMA2]	2E-135 3E-135	YP_007002604.1 YP_002154290.1
PA1P1_076c	54358 - 53327	58.4	343	putative 3'-phosphatase, 5'-polynucleotide kinase [<i>Pseudomonas aeruginosa</i>] putative polynucleotide kinase [<i>Pseudomonas</i> phage KPP12]	0 0	SBT96767.1 YP_007238211.1
PA1P1_077c	54552 - 54361	48.4	63	hypothetical protein PJG24_060 [<i>Pseudomonas</i> phage JG024] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	3E-35 1E-34	YP_006200824.1 YP_007238212.1
PA1P1_078c	55471 - 54554	58.6	305	putative thymidylate synthase [<i>Pseudomonas</i> phage JG024] hypothetical protein PP141_gp60 [<i>Pseudomonas</i> phage 14-1]	0 0	YP_006200825.1 YP_002364368.1
PA1P1_079c	55677 - 55471	52.2	68	hypothetical protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein SL1_42 [<i>Pseudomonas</i> phage SL1]	1E-40 2E-40	YP_007238214.1 AUS03317.1
PA1P1_080c	55951 - 55685	56.9	88	hypothetical protein [<i>Pseudomonas</i> phage PA5] hypothetical protein phiKT28_064 [<i>Pseudomonas</i> phage phiKT28]	2E-56 5E-56	APD20761.1 AKJ71502.1

PA1P1_081c	56169 - 55951	55.7	72	hypothetical protein PPSN_gp64 [<i>Pseudomonas</i> phage SN] hypothetical protein LMA2_gp62 [<i>Pseudomonas</i> phage LMA2]	2E-46 3E-46	YP_002418870.1 YP_002154296.1
PA1P1_082c	56371 - 56153	59.8	72	hypothetical protein LBL3_gp61 [<i>Pseudomonas</i> phage LBL3] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	5E-43 2E-42	YP_002154206.1 YP_007238217.1
PA1P1_083c	56601 - 56371	58.9	76	hypothetical protein PP141_gp65 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp62 [<i>Pseudomonas</i> phage LBL3]	6E-50 1E-49	YP_002364373.1 YP_002154207.1
PA1P1_084c	57691 - 56690	56.2	333	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein vB_Pae_PS44_00069 [<i>Pseudomonas</i> phage vB_Pae_PS44]	0 0	YP_009215162.1 YP_009211393.1
PA1P1_085c	58680 - 57796	62.1	294	hypothetical protein PP141_gp67 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	0 0	YP_002364375.1 YP_009215161.1
PA1P1_086c	60029 - 58842	55.4	395	putative ATP-dependent exonuclease V [<i>Pseudomonas</i> phage SN] hypothetical protein ORF067 [<i>Pseudomonas</i> phage F8]	0 0	YP_002418875.1 YP_001294484.1
PA1P1_087c	60438 - 60016	57.0	140	hypothetical protein ORF068 [<i>Pseudomonas</i> phage F8] hypothetical protein [<i>Pseudomonas</i> phage NP3]	3E-98 1E-97	YP_001294485.1 AMQ76187.1
PA1P1_088	60607 - 61392	59.2	261	hypothetical protein PP141_gp70 [<i>Pseudomonas</i> phage 14-1] hypothetical protein ORF069 [<i>Pseudomonas</i> phage F8]	0 0	YP_002364378.1 YP_001294486.1
PA1P1_089	61403 - 62626	59.1	407	hypothetical protein vBPaeME215_00050 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein LBL3_gp68 [<i>Pseudomonas</i> phage LBL3]	0 0	ASZ72528.1 YP_002154213.1
PA1P1_090	62650 - 63099	58.2	149	hypothetical protein PP141_gp72 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage NP3]	3E-105 5E-105	YP_002364380.1 AMQ76190.1
PA1P1_091	63096 - 64172	57.7	358	hypothetical protein [<i>Pseudomonas</i> phage DL52] hypothetical protein PP141_gp73 [<i>Pseudomonas</i> phage 14-1]	0 0	AKF13701.1 YP_002364381.1
PA1P1_092	64178 - 64363	47.8	61	hypothetical protein ORF073 [<i>Pseudomonas</i> phage F8] hypothetical protein phiKT28_076 [<i>Pseudomonas</i> phage phiKT28]	4E-33 3E-32	YP_001294490.1 AKJ71514.1
PA1P1_093	64511 - 66250	53.3	579	putative Ploop ATPase [<i>Pseudomonas aeruginosa</i>] virulence-associated protein E [<i>Pseudomonas</i> phage vB_Pae_PS44]	0 0	SBT96795.1 YP_009211402.1

Table S5: Predicted genes of *P. aeruginosa* phage PA8P1. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC (%)	Protein length (aa)	Amino acid sequence identity/similarity to best homologs (% amino acid identity)	E-value (BLAST)	Accession no.
PA8P1_001	601 - 1170	59.1	189	hypothetical protein PP141_gp76 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage S12-1]	4E-138 1E-137	YP_002364384.1 BAU16489.1
PA8P1_002c	1949 - 1338	54.7	203	hypothetical protein vBPaeME215_00056 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein PP141_gp77 [<i>Pseudomonas</i> phage 14-1]	3E-142 6E-142	ASZ72534.1 YP_002364385.1
PA8P1_003c	2834 - 2139	60.5	231	hypothetical protein PP141_gp78 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeME215_00057 [<i>Pseudomonas</i> phage vB_PaeM_E215]	2E-166 5E-166	YP_002364386.1 ASZ72535.1
PA8P1_004c	3156 - 2845	56.1	103	hypothetical protein PP141_gp79 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeME217_00082 [<i>Pseudomonas</i> phage vB_PaeM_E217]	1E-72 6E-72	YP_002364387.1 ASZ72466.1
PA8P1_005c	3427 - 3206	53.2	73	hypothetical protein I7A_082c [<i>Pseudomonas</i> phage NH-4] hypothetical protein PP141_gp80 [<i>Pseudomonas</i> phage 14-1]	2E-44 5E-44	YP_007002628.1 YP_002364388.1

PA8P1_006c	3707 - 3483	54.7	74	hypothetical protein PPSN_gp83 [<i>Pseudomonas</i> phage SN] hypothetical protein LBL3_gp79 [<i>Pseudomonas</i> phage LBL3]	4E-47 2E-46	YP_002418889.1 YP_002154224.1
PA8P1_007c	4099 - 3773	56.3	108	hypothetical protein PII10A_07 [<i>Pseudomonas aeruginosa</i>] hypothetical protein LBL3_gp80 [<i>Pseudomonas</i> phage LBL3]	7E-74 2E-73	SBT96689.1 YP_002154225.1
PA8P1_008c	4744 - 4100	59.7	214	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_088 [<i>Pseudomonas</i> phage JG024]	2E-154 4E-154	YP_009215144.1 YP_006200852.1
PA8P1_009c	4985 - 4776	58.6	69	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	7E-45 7E-40	WP_015994944.1 YP_009124313.1
PA8P1_010c	5197 - 4982	52.3	71	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_090 [<i>Pseudomonas</i> phage JG024]	7E-44 3E-43	YP_009215142.1 YP_006200854.1
PA8P1_011c	5394 - 5194	56.7	66	hypothetical protein [<i>Pseudomonas</i> phage KPP22] hypothetical protein vBPaeMDP1_0085 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	2E-39 2E-39	BAU20627.1 AKP24472.1
PA8P1_012c	5642 - 5391	51.6	83	hypothetical protein vBPaeME217_00092 [<i>Pseudomonas</i> phage vB_PaeM_E217] hypothetical protein I7A_091c [<i>Pseudomonas</i> phage NH-4]	1E-53 2E-53	ASZ72476.1 YP_007002637.1
PA8P1_013c	5917 - 5729	54.5	62	hypothetical protein PJG24_093 [<i>Pseudomonas</i> phage JG024] hypothetical protein [<i>Pseudomonas</i> phage DL68]	8E-36 7E-35	YP_006200857.1 YP_009215139.1
PA8P1_014c	6642 - 5920	55.6	240	hypothetical protein PJG24_094 [<i>Pseudomonas</i> phage JG024] hypothetical protein BrSP1_16 [<i>Pseudomonas</i> phage BrSP1]	3E-166 5E-165	YP_006200858.1 ATI16268.1
PA8P1_015c	6963 - 6661	54.1	100	hypothetical protein vBPaeMDP1_0001 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1] hypothetical protein PJG24_001 [<i>Pseudomonas</i> phage JG024]	1E-63 3E-63	AKP24388.1 YP_006200766.1
PA8P1_016c	7192 - 7019	53.4	57	hypothetical protein PPSN_gp02 [<i>Pseudomonas</i> phage SN] hypothetical protein PII10A_17 [<i>Pseudomonas aeruginosa</i>]	5E-34 1E-33	YP_002418808.1 SBT96699.1
PA8P1_017c	7389 - 7243	53.1	48	hypothetical protein PPSN_gp03 [<i>Pseudomonas</i> phage SN] hypothetical protein SAMN05216409_118116 [<i>Pseudomonas lutea</i>]	5E-23 6E-13	YP_002418809.1 SER37912.1
PA8P1_018	7437 - 7559	49.6	40	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp01 [<i>Pseudomonas</i> phage LBL3]	2E-19 8E-13	YP_009215134.1 YP_002154146.1
PA8P1_019	7564 - 8946	52.4	460	terminase large subunit [<i>Pseudomonas</i> phage DL68] large terminase protein [<i>Pseudomonas</i> phage vB_PaeM_E215]	0 0	YP_009215133.1 ASZ72553.1
PA8P1_020c	9366 - 8983	59.1	127	hypothetical protein PP141_gp04 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage NP3]	3E-86 7E-86	YP_002364312.1 AMQ76120.1
PA8P1_021c	9581 - 9363	54.8	72	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage NP3]	4E-46 3E-45	WP_015994883.1 AMQ76121.1
PA8P1_022c	9931 - 9581	60.7	116	hypothetical protein LBL3_gp05 [<i>Pseudomonas</i> phage LBL3] hypothetical protein SL1_06 [<i>Pseudomonas</i> phage SL1]	1E-78 2E-76	YP_002154150.1 AUS03281.1
PA8P1_023c	10373 - 9975	59.4	132	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein LBL3_gp06 [<i>Pseudomonas</i> phage LBL3]	1E-87 2E-86	YP_009215129.1 YP_002154151.1
PA8P1_024c	11155 - 10376	57.2	259	hypothetical protein PP141_gp08 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	0 0	YP_002364316.1 YP_009215128.1
PA8P1_025c	11679 - 11242	60.3	145	hypothetical protein vB_Pae436M-8_10 [<i>Pseudomonas</i> phage vB_Pae436M-8] hypothetical protein [<i>Pseudomonas</i> phage NP3]	2E-98 2E-97	ANT44196.1 AMQ76125.1
PA8P1_026c	12283 - 11696	56.8	195	Phage protein [<i>Pseudomonas</i> phage S12-1] hypothetical protein LBL3_gp09 [<i>Pseudomonas</i> phage LBL3]	6E-145 1E-144	BAU16423.1 YP_002154154.1
PA8P1_027c	12388 - 12293	51.0	31	hypothetical protein PP141_gp11 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp88 [<i>Pseudomonas</i> phage LBL3]	2E-11 3E-11	YP_002364319.1 YP_004221739.1
PA8P1_028c	13317 - 12385	56.6	310	hypothetical protein PP141_gp12 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeME215_00085 [<i>Pseudomonas</i> phage vB_PaeM_E215]	0 0	YP_002364320.1 ASZ72563.1
PA8P1_029c	13920 - 13420	56.3	166	hypothetical protein PP141_gp13 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PJG24_013 [<i>Pseudomonas</i> phage JG024]	4E-120 2E-119	YP_002364321.1 YP_006200778.1
PA8P1_030c	14287 - 13940	54.0	115	hypothetical protein PP141_gp14 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	9E-76 1E-75	YP_002364322.1 YP_009215123.1
PA8P1_031c	14847 - 14536	50.3	103	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_015 [<i>Pseudomonas</i> phage JG024]	4E-67 3E-66	YP_009215122.1 YP_006200780.1

PA8P1_032c	15056 - 14853	56.4	67	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PPGF8SP_0081 [Pseudomonas phage SPM-1]	2E-39 4E-37	YP_009215121.1 AHH02940.1
PA8P1_033c	15376 - 15053	56.2	107	hypothetical protein vBPaeME215_00090 [Pseudomonas phage vB_PaeM_E215] hypothetical protein vB_Pae_PS44_00019 [Pseudomonas phage vB_Pae_PS44]	9E-75 5E-74	ASZ72568.1 YP_009211343.1
PA8P1_034c	15808 - 15407	53.0	133	hypothetical protein vBPaeME215_00091 [Pseudomonas phage vB_PaeM_E215] hypothetical protein PP141_gp17 [Pseudomonas phage 14-1]	1E-92 1E-91	ASZ72569.1 YP_002364325.1
PA8P1_035	15988 - 18285	56.7	765	hypothetical protein [Pseudomonas phage DL68] hypothetical protein vBPaeME215_00092 [Pseudomonas phage vB_PaeM_E215]	0 0	YP_009215210.1 ASZ72570.1
PA8P1_036	18285 - 19121	53.4	278	hypothetical protein PP141_gp19 [Pseudomonas phage 14-1] putative minor head protein [Pseudomonas phage KPP12]	0 0	YP_002364327.1 YP_007238173.1
PA8P1_037	19140 - 19346	55.1	68	hypothetical protein phiKT28_022 [Pseudomonas phage phiKT28] hypothetical protein vBPaeMDP1_0020 [Pseudomonas phage vB_PaeM_CEB_DP1]	1E-41 5E-41	AKJ71460.1 AKP24407.1
PA8P1_038	19343 - 19483	53.2	46	hypothetical protein LMA2_gp20 [Pseudomonas phage LMA2] hypothetical protein BrSP1_38 [Pseudomonas phage BrSP1]	2E-23 9E-23	YP_002154254.1 ATI16221.1
PA8P1_039	20035 - 21429	58.2	464	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PP141_gp22 [Pseudomonas phage 14-1]	0 0	YP_009215206.1 YP_002364330.1
PA8P1_040	21433 - 22068	62.7	211	hypothetical protein PP141_gp23 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage SN]	5E-148 1E-147	YP_002364331.1 YP_002418830.1
PA8P1_041	22078 - 23226	61.3	382	capsid and scaffold protein [Pseudomonas phage NP3] putative major structural protein [Pseudomonas phage vB_PaeM_CEB_DP1]	0 0	AMQ76141.1 AKP24411.1
PA8P1_042	23328 - 23765	54.1	145	hypothetical protein PPSN_gp26 [Pseudomonas phage SN] hypothetical protein LBL3_gp22 [Pseudomonas phage LBL3]	1E-103 3E-103	YP_002418832.1 YP_002154167.1
PA8P1_043	23780 - 24247	58.3	155	structural protein [Pseudomonas phage SN] hypothetical protein [Pseudomonas phage DL68]	2E-109 3E-109	YP_002418833.1 YP_009215202.1
PA8P1_044	24244 - 24642	51.4	132	hypothetical protein [Pseudomonas phage NP3] structural protein [Pseudomonas phage SN]	3E-92 8E-92	AMQ76144.1 YP_002418834.1
PA8P1_045	24650 - 25201	48.0	183	hypothetical protein LBL3_gp25 [Pseudomonas phage LBL3] hypothetical protein LMA2_gp27 [Pseudomonas phage LMA2]	9E-133 1E-132	YP_002154170.1 YP_002154261.1
PA8P1_046	25198 - 25779	54.8	193	hypothetical protein ORF028 [Pseudomonas phage F8] hypothetical protein [Pseudomonas phage KPP12]	3E-137 1E-136	YP_001294445.1 YP_007238183.1
PA8P1_047	25795 - 27309	59.5	504	hypothetical protein I7A_031 [Pseudomonas phage NH-4] hypothetical protein vBPaeMDP1_0030 [Pseudomonas phage vB_PaeM_CEB_DP1]	0 0	YP_007002577.1 AKP24417.1
PA8P1_048	27368 - 27820	59.8	150	putative structural protein [Pseudomonas phage LMA2] structural protein [Pseudomonas phage phiKT28]	2E-103 2E-102	YP_002154264.1 AKJ71471.1
PA8P1_049	27820 - 28143	54.6	107	putative structural protein [Pseudomonas phage LMA2] putative structural protein [Pseudomonas phage JG024]	2E-75 5E-75	YP_002154265.1 YP_006200797.1
PA8P1_050	28140 - 28490	53.6	116	putative structural protein [Pseudomonas phage LMA2] structural protein [Pseudomonas phage SL1]	3E-78 1E-77	YP_002154266.1 AUS03345.1
PA8P1_051	28492 - 28923	65.0	143	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PPSN_gp35 [Pseudomonas phage SN]	3E-92 1E-91	YP_009215194.1 YP_002418841.1
PA8P1_052	28933 - 29436	52.2	167	structural protein [Pseudomonas phage SN] putative structural protein [Pseudomonas phage LMA2]	3E-115 1E-114	YP_002418842.1 YP_002154268.1
PA8P1_053	29436 - 29975	55.7	179	putative structural protein [Pseudomonas phage LMA2] putative structural protein [Pseudomonas phage LBL3]	3E-127 9E-127	YP_002154269.1 YP_002154178.1
PA8P1_054	29984 - 30577	46.6	197	hypothetical protein vBPaeME217_00038 [Pseudomonas phage vB_PaeM_E217] putative structural protein [Pseudomonas phage KPP12]	5E-140 2E-139	ASZ72422.1 YP_007238190.1
PA8P1_055	30587 - 31015	57.1	142	hypothetical protein LBL3_gp35 [Pseudomonas phage LBL3] hypothetical protein phiKTN6_037 [Pseudomonas phage phiKTN6]	4E-101 2E-100	YP_002154180.1 AKJ71569.1
PA8P1_056	31019 - 33595	57.9	858	putative lytic tail protein [Pseudomonas phage LMA2] internal (core) protein [Pseudomonas phage NP3]	0 0	YP_002154272.1 AMQ76156.1
PA8P1_057	33595 - 34458	51.7	287	putative structural protein [Pseudomonas phage LMA2] putative structural protein [Pseudomonas phage vB_PaeM_CEB_DP1]	0 0	YP_002154273.1 AKP24427.1
PA8P1_058	34458 - 34991	47.8	177	hypothetical protein PP141_gp41 [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage DL68]	2E-127 5E-127	YP_002364349.1 YP_009215187.1

PA8P1_059	35047 - 35712	53.0	221	hypothetical protein LMA2_gp41 [<i>Pseudomonas</i> phage LMA2] putative baseplate [<i>Pseudomonas</i> phage KPP12]	2E-160 4E-160	YP_002154275.1 YP_007238195.1
PA8P1_060A	35723 - 35776	42.6	17	hypothetical protein PB1_gp43 [<i>Pseudomonas</i> phage PB1] putative baseplate protein [<i>Pseudomonas</i> phage SN]	3E-09 2E-04	YP_002455973.1 YP_002418850.1
PA8P1_060B	35769 - 37022	57.7	417	putative structural protein [<i>Pseudomonas</i> phage LMA2] putative baseplate protein [<i>Pseudomonas</i> phage SN]	0 0	YP_002154276.1 YP_002418850.1
PA8P1_061	37019 - 38533	56.0	504	hypothetical protein PP141_gp44 [<i>Pseudomonas</i> phage 14-1] structural protein [<i>Pseudomonas</i> phage vB_Pae436M-8]	0 0	YP_002364352.1 ANT44230.1
PA8P1_062	38538 - 41426	57.1	962	putative tail fiber component [<i>Pseudomonas</i> phage NH-4] tail fibers protein [<i>Pseudomonas</i> phage NP3]	0 0	YP_007002592.1 AMQ76163.1
PA8P1_063	41428 - 41856	58.3	142	hypothetical protein [<i>Pseudomonas</i> phage NP3] putative tail fiber component [<i>Pseudomonas</i> phage JG024]	9E-99 2E-97	AMQ76164.1 YP_006200811.1
PA8P1_064	41856 - 42518	60.5	220	lytic enzyme [<i>Pseudomonas</i> phage NP3] putative endolysin [<i>Pseudomonas</i> phage JG024]	2E-161 7E-161	AMQ76165.1 YP_006200812.1
PA8P1_065c	42793 - 42542	51.2	83	hypothetical protein PP141_gp48 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LMA2_gp47 [<i>Pseudomonas</i> phage LMA2]	2E-50 3E-50	YP_002364356.1 YP_002154281.1
PA8P1_066c	43984 - 43073	55.7	303	DNA ligase [<i>Pseudomonas</i> phage phiKT28] putative DNA ligase [<i>Pseudomonas</i> phage JG024]	0 0	AKJ71489.1 YP_006200814.1
PA8P1_067c	44593 - 44039	54.4	184	DNA binding protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_051 [<i>Pseudomonas</i> phage JG024]	2E-132 2E-131	YP_009215178.1 YP_006200815.1
PA8P1_068c	45195 - 44590	60.2	201	hypothetical protein ORF050 [<i>Pseudomonas</i> phage F8] hypothetical protein PP141_gp51 [<i>Pseudomonas</i> phage 14-1]	4E-139 9E-139	YP_001294467.1 YP_002364359.1
PA8P1_069c	46148 - 45249	59.9	299	hypothetical protein PP141_gp52 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage DL68]	0 0	YP_002364360.1 YP_009215176.1
PA8P1_070c	46857 - 46237	53.3	206	hypothetical protein vBPaeMLS1_79 [<i>Pseudomonas</i> phage vB_PaeM_LS1] hypothetical protein SL1_50 [<i>Pseudomonas</i> phage SL1]	3E-145 1E-144	AVI48847.1 AUS03325.1
PA8P1_071c	48511 - 46952	55.1	519	hypothetical protein PPSN_gp55 [<i>Pseudomonas</i> phage SN] DNA helicase [<i>Pseudomonas</i> phage vB_Pae436M-8]	0 0	YP_002418861.1 ANT44241.1
PA8P1_072c	48918 - 48508	55.2	136	hypothetical protein LBL3_gp52 [<i>Pseudomonas</i> phage LBL3] hypothetical protein [<i>Pseudomonas</i> phage NP3]	6E-95 6E-95	YP_002154197.1 AMQ76173.1
PA8P1_073c	52018 - 48911	54.9	1035	hypothetical protein PP141_gp56 [<i>Pseudomonas</i> phage 14-1] DNA polymerase III subunit alpha [<i>Pseudomonas</i> phage vB_Pae_PS44]	0 0	YP_002364364.1 YP_009211383.1
PA8P1_074c	52572 - 52018	52.8	184	putative DNA polymerase III, epsilon subunit [<i>Pseudomonas</i> phage LMA2] putative DNA polymerase III epsilon subunit [<i>Pseudomonas</i> phage NH-4]	3E-135 3E-135	YP_002154290.1 YP_007002604.1
PA8P1_075c	53679 - 52648	58.4	343	putative 3'-phosphatase, 5'-polynucleotide kinase [<i>Pseudomonas aeruginosa</i>] putative polynucleotide kinase [<i>Pseudomonas</i> phage KPP12]	0 0	SBT96767.1 YP_007238211.1
PA8P1_076c	53873 - 53682	49.0	63	hypothetical protein PJG24_060 [<i>Pseudomonas</i> phage JG024] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	3E-35 1E-34	YP_006200824.1 YP_007238212.1
PA8P1_077c	54792 - 53875	58.1	305	hypothetical protein PP141_gp60 [<i>Pseudomonas</i> phage 14-1] putative thymidylate synthase [<i>Pseudomonas</i> phage JG024]	0 0	YP_002364368.1 YP_006200825.1
PA8P1_078c	54998 - 54792	50.1	68	hypothetical protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein SL1_42 [<i>Pseudomonas</i> phage SL1]	4E-41 8E-41	YP_007238214.1 AUS03317.1
PA8P1_079c	55236 - 55006	57.1	76	hypothetical protein PPSN_gp63 [<i>Pseudomonas</i> phage SN] hypothetical protein PP141_gp62 [<i>Pseudomonas</i> phage 14-1]	1E-47 1E-47	YP_002418869.1 YP_002364370.1
PA8P1_080c	55487 - 55269	54.8	72	hypothetical protein PPSN_gp64 [<i>Pseudomonas</i> phage SN] hypothetical protein LMA2_gp62 [<i>Pseudomonas</i> phage LMA2]	2E-46 3E-46	YP_002418870.1 YP_002154296.1
PA8P1_081c	55689 - 55471	59.4	72	hypothetical protein LBL3_gp61 [<i>Pseudomonas</i> phage LBL3] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	2E-42 6E-42	YP_002154206.1 YP_007238217.1
PA8P1_082c	55919 - 55689	58.9	76	hypothetical protein PP141_gp65 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp62 [<i>Pseudomonas</i> phage LBL3]	6E-50 1E-49	YP_002364373.1 YP_002154207.1
PA8P1_083c	57008 - 56007	55.6	333	hypothetical protein PP141_gp66 [<i>Pseudomonas</i> phage 14-1] hypothetical protein PB1_gp68 [<i>Pseudomonas</i> phage PB1]	0 0	YP_002364374.1 YP_002455998.1

PA8P1_084c	58003 - 57113	63.2	296	hypothetical protein [<i>Pseudomonas</i> phage PA5] putative structural protein [<i>Pseudomonas</i> phage KPP12]	1E-169 2E-169	APD20755.1 YP_007238220.1
PA8P1_085c	59351 - 58164	55.0	395	putative ATP-dependent exonuclease V [<i>Pseudomonas</i> phage SN] hypothetical protein ORF067 [<i>Pseudomonas</i> phage F8]	0 0	YP_002418875.1 YP_001294484.1
PA8P1_086c	59760 - 59338	56.7	140	hypothetical protein ORF068 [<i>Pseudomonas</i> phage F8] hypothetical protein I7A_070c [<i>Pseudomonas</i> phage NH-4]	1E-97 3E-97	YP_001294485.1 YP_007002616.1
PA8P1_087	59929 - 60714	59.0	261	hypothetical protein LMA2_gp69 [<i>Pseudomonas</i> phage LMA2] hypothetical protein vBPaeMLS1_62 [<i>Pseudomonas</i> phage vB_PaeM_LS1]	0 0	YP_002154303.1 AVJ48831.1
PA8P1_088	60725 - 61726	57.6	333	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein vB_Pae436M-8_72 [<i>Pseudomonas</i> phage vB_Pae436M-8]	2E-92 5E-77	WP_051488611.1 ANT44258.1
PA8P1_089	61726 - 62175	58.2	149	hypothetical protein [<i>Pseudomonas</i> phage DL60] hypothetical protein [<i>Pseudomonas</i> phage NP3]	7E-104 9E-103	YP_009193759.1 AMQ76190.1
PA8P1_090	62172 - 63248	57.5	358	hypothetical protein PP141_gp73 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeMLS1_59 [<i>Pseudomonas</i> phage vB_PaeM_LS1]	0 0	YP_002364381.1 AVJ48828.1
PA8P1_091	63254 - 63439	50.5	61	hypothetical protein LMA2_gp73 [<i>Pseudomonas</i> phage LMA2] hypothetical protein PPSN_gp75 [<i>Pseudomonas</i> phage SN]	9E-34 2E-33	YP_002154307.1 YP_002418881.1
PA8P1_092	63587 - 65326	53.3	579	putative Ploop ATPase [<i>Pseudomonas aeruginosa</i>] virulence-associated protein E [<i>Pseudomonas</i> phage vB_Pae_PS44]	0 0	SBT96795.1 YP_009211402.1

Table S6: Predicted genes of *P. aeruginosa* phage PA11P1. Homologs were achieved from BLASTp analyzes.

Locus tag	Position	GC (%)	Protein length (aa)	Amino acid sequence identity/similarity to best homologs (% amino acid identity)	E-value (BLAST)	Accession no.
PA11P1_001	604 - 1173	58.9	189	hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27] hypothetical protein LMA2_gp76 [<i>Pseudomonas</i> phage LMA2]	5E-138 5E-137	YP_009124304.1 YP_002154309.1
PA11P1_002c	1952 - 1341	55.1	203	hypothetical protein vBPaeME215_00056 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein PP141_gp77 [<i>Pseudomonas</i> phage 14-1]	2E-143 5E-143	ASZ72534.1 YP_002364385.1
PA11P1_003c	2828 - 2142	60.0	228	hypothetical protein PP141_gp78 [<i>Pseudomonas</i> phage 14-1] hypothetical protein vBPaeME215_00057 [<i>Pseudomonas</i> phage vB_PaeM_E215]	3E-157 1E-156	YP_002364386.1 ASZ72535.1
PA11P1_004c	3150 - 2839	55.8	103	hypothetical protein vBPaeMDP1_0076 [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1] hypothetical protein BrSP1_5 [<i>Pseudomonas</i> phage BrSP1]	1E-71 4E-71	AKP24463.1 ATI16257.1
PA11P1_005c	3424 - 3203	52.7	73	hypothetical protein PP141_gp80 [<i>Pseudomonas</i> phage 14-1] hypothetical protein I7A_082c [<i>Pseudomonas</i> phage NH-4]	3E-44 5E-44	YP_002364388.1 YP_007002628.1
PA11P1_006c	3688 - 3434	56.9	84	hypothetical protein PP141_gp81 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage KPP22]	1E-53 5E-49	YP_002364389.1 BAU20633.1
PA11P1_007c	3966 - 3742	55.6	74	hypothetical protein LBL3_gp79 [<i>Pseudomonas</i> phage LBL3] hypothetical protein PPSN_gp83 [<i>Pseudomonas</i> phage SN]	3E-47 2E-46	YP_002154224.1 YP_002418889.1
PA11P1_008c	4358 - 4032	56.3	108	hypothetical protein PII10A_07 [<i>Pseudomonas aeruginosa</i>] hypothetical protein LBL3_gp80 [<i>Pseudomonas</i> phage LBL3]	7E-74 2E-73	SBT96689.1 YP_002154225.1
PA11P1_009c	5003 - 4359	59.7	214	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_088 [<i>Pseudomonas</i> phage JG024]	2E-154 4E-154	YP_009215144.1 YP_006200852.1
PA11P1_010c	5244 - 5035	58.6	69	hypothetical protein [<i>Pseudomonas aeruginosa</i>] hypothetical protein [<i>Pseudomonas</i> phage vB_PaeM_PAO1_Ab27]	7E-45 7E-40	WP_015994944.1 YP_009124313.1
PA11P1_011c	5456 - 5241	52.3	71	hypothetical protein [<i>Pseudomonas</i> phage DL68] hypothetical protein PJG24_090 [<i>Pseudomonas</i> phage JG024]	7E-44 3E-43	YP_009215142.1 YP_006200854.1

PA11P1_012c	5653 - 5453	56.7	66	hypothetical protein [Pseudomonas phage KPP22] hypothetical protein vBPaeMDP1_0085 [Pseudomonas phage vB_PaeM_CEB_DP1]	2E-39 2E-39	BAU20627.1 BAU16501.1
PA11P1_013c	5901 - 5650	51.6	83	hypothetical protein vBPaeME217_00092 [Pseudomonas phage vB_PaeM_E217] hypothetical protein I7A_091c [Pseudomonas phage NH-4]	1E-53 2E-53	ASZ72476.1 YP_007002637.1
PA11P1_014c	6176 - 5988	54.5	62	hypothetical protein PJG24_093 [Pseudomonas phage JG024] hypothetical protein [Pseudomonas phage DL68]	8E-36 7E-35	YP_006200857.1 YP_009215139.1
PA11P1_015c	6865 - 6179	55.7	228	hypothetical protein PJG24_094 [Pseudomonas phage JG024] hypothetical protein BrSP1_16 [Pseudomonas phage BrSP1]	3E-166 5E-165	YP_006200858.1 ATI16268.1
PA11P1_016c	7222 - 6920	54.1	100	hypothetical protein vBPaeMDP1_0001 [Pseudomonas phage vB_PaeM_CEB_DP1] hypothetical protein PJG24_001 [Pseudomonas phage JG024]	1E-63 3E-63	AKP24388.1 YP_006200766.1
PA11P1_017c	7451 - 7278	53.4	57	hypothetical protein PPSN_gp02 [Pseudomonas phage SN] hypothetical protein PII10A_17 [Pseudomonas aeruginosa]	5E-34 1E-33	YP_002418808.1 SBT96699.1
PA11P1_018c	7648 - 7502	53.1	48	hypothetical protein PPSN_gp03 [Pseudomonas phage SN] hypothetical protein SAMN05216409_118116 [Pseudomonas lutea]	6E-23 6E-13	YP_002418809.1 SER37912.1
PA11P1_019	7823 - 9205	52.4	460	terminase large subunit [Pseudomonas phage DL68] large terminase protein [Pseudomonas phage vB_PaeM_E215]	0 0	YP_009215133.1 ASZ72553.1
PA11P1_020c	9625 - 9242	59.1	127	hypothetical protein PP141_gp04 [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage NP3]	3E-86 7E-86	YP_002364312.1 AMQ76120.1
PA11P1_021c	9840 - 9622	54.8	72	hypothetical protein [Pseudomonas aeruginosa] hypothetical protein [Pseudomonas phage NP3]	4E-46 3E-45	WP_015994883.1 AMQ76121.1
PA11P1_022c	10190 - 9840	60.7	116	hypothetical protein LBL3_gp05 [Pseudomonas phage LBL3] hypothetical protein SL1_06 [Pseudomonas phage SL1]	1E-78 2E-76	YP_002154150.1 AUS03281.1
PA11P1_023c	10632 - 10234	59.4	132	hypothetical protein [Pseudomonas phage DL68] hypothetical protein LBL3_gp06 [Pseudomonas phage LBL3]	1E-87 2E-86	YP_009215129.1 YP_002154151.1
PA11P1_024c	11414 - 10635	57.2	259	hypothetical protein PP141_gp08 [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage DL68]	0 0	YP_002364316.1 YP_009215128.1
PA11P1_025c	11938 - 11501	60.3	145	hypothetical protein vB_Pae436M-8_10 [Pseudomonas phage vB_Pae436M-8] hypothetical protein [Pseudomonas phage NP3]	2E-98 2E-97	ANT44196.1 AMQ76125.1
PA11P1_026c	12542 - 11955	56.8	195	Phage protein [Pseudomonas phage S12-1] hypothetical protein LBL3_gp09 [Pseudomonas phage LBL3]	6E-145 1E-144	BAU16423.1 YP_002154154.1
PA11P1_027c	12647 - 12552	51.0	31	hypothetical protein PP141_gp11 [Pseudomonas phage 14-1] hypothetical protein LBL3_gp88 [Pseudomonas phage LBL3]	2E-11 3E-11	YP_002364319.1 YP_004221739.1
PA11P1_028c	13576 - 12644	56.6	310	hypothetical protein PP141_gp12 [Pseudomonas phage 14-1] hypothetical protein vBPaeME215_00085 [Pseudomonas phage vB_PaeM_E215]	0 0	YP_002364320.1 ASZ72563.1
PA11P1_029c	14179 - 13679	56.3	166	hypothetical protein PP141_gp13 [Pseudomonas phage 14-1] hypothetical protein PJG24_013 [Pseudomonas phage JG024]	4E-120 1E-119	YP_002364321.1 YP_006200778.1
PA11P1_030c	14546 - 14199	54.0	115	hypothetical protein PP141_gp14 [Pseudomonas phage 14-1] hypothetical protein [Pseudomonas phage DL68]	9E-76 1E-75	YP_002364322.1 YP_009215123.1
PA11P1_031c	15106 - 14795	50.3	103	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PJG24_015 [Pseudomonas phage JG024]	4E-67 3E-66	YP_009215122.1 YP_006200780.1
PA11P1_032c	15315 - 15112	56.4	67	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PPGF8SP_0081 [Pseudomonas phage SPM-1]	2E-39 4E-37	YP_009215121.1 AHH02940.1
PA11P1_033c	15635 - 15312	56.2	107	hypothetical protein vBPaeME215_00090 [Pseudomonas phage vB_PaeM_E215] hypothetical protein vB_Pae_PS44_00019 [Pseudomonas phage vB_Pae_PS44]	9E-75 5E-74	ASZ72568.1 YP_009211343.1

PA11P1_034c	16067 - 15666	53.0	133	hypothetical protein vBPaeME215_00091 [Pseudomonas phage vB_PaeM_E215] hypothetical protein PP141_gp17 [Pseudomonas phage 14-1]	1E-92 1E-91	ASZ72569.1 YP_002364325.1
PA11P1_035	16247 - 18544	56.8	729	hypothetical protein [Pseudomonas phage DL68] hypothetical protein vBPaeME215_00092 [Pseudomonas phage vB_PaeM_E215]	0 0	YP_009215210.1 ASZ72570.1
PA11P1_036	18544 - 19380	53.4	278	putative minor head protein [Pseudomonas phage SN] putative minor head protein [Pseudomonas phage SL1]	0 0	YP_002418826.1 AUS03359.1
PA11P1_037	19399 - 19605	55.6	68	hypothetical protein PPSN_gp21 [Pseudomonas phage SN] hypothetical protein LBL3_gp17 [Pseudomonas phage LBL3]	2E-41 6E-40	YP_002418827.1 YP_002154162.1
PA11P1_038	19602 - 19742	53.2	46	hypothetical protein PPSN_gp22 [Pseudomonas phage SN] hypothetical protein PJG24_021 [Pseudomonas phage JG024]	4E-23 3E-22	YP_002418828.1 YP_006200786.1
PA11P1_039	20296 - 21690	58.3	464	hypothetical protein [Pseudomonas phage DL68] hypothetical protein PP141_gp22 [Pseudomonas phage 14-1]	0 0	YP_009215206.1 YP_002364330.1
PA11P1_040	21694 - 22329	62.6	211	hypothetical protein PP141_gp23 [Pseudomonas phage 14-1] structural protein [Pseudomonas phage SN]	5E-148 1E-147	YP_002364331.1 YP_002418830.1
PA11P1_041	22339 - 23487	61.0	382	putative major structural protein [Pseudomonas phage vB_PaeM_CEB_DP1] hypothetical protein PP141_gp24 [Pseudomonas phage 14-1]	0 0	AKP24411.1 YP_002364332.1
PA11P1_042	23589 - 24026	55.0	145	hypothetical protein vBPaeMDP1_0025 [Pseudomonas phage vB_PaeM_CEB_DP1] hypothetical protein [Pseudomonas phage KPP12]	6E-104 2E-103	AKP24412.1 YP_007238179.1
PA11P1_043	24041 - 24508	59.2	155	putative structural protein [Pseudomonas phage KPP12] structural protein [Pseudomonas phage phiKTN6]	4E-110 1E-109	YP_007238180.1 AKJ71557.1
PA11P1_044	24505 - 24903	52.1	132	putative structural protein [Pseudomonas phage KPP12] structural protein [Pseudomonas phage phiKTN6]	2E-91 6E-91	YP_007238181.1 AKJ71558.1
PA11P1_045	24911 - 25462	48.6	183	hypothetical protein [Pseudomonas phage KPP12] hypothetical protein vB_Pae_PS44_00031 [Pseudomonas phage vB_Pae_PS44]	3E-133 5E-133	YP_007238182.1 YP_009211355.1
PA11P1_046	25459 - 26040	54.8	193	hypothetical protein ORF028 [Pseudomonas phage F8] hypothetical protein [Pseudomonas phage KPP12]	3E-137 1E-136	YP_001294445.1 YP_007238183.1
PA11P1_047	26056 - 27570	59.1	504	hypothetical protein I7A_031 [Pseudomonas phage NH-4] hypothetical protein vBPaeMDP1_0030 [Pseudomonas phage vB_PaeM_CEB_DP1]	0 0	YP_007002577.1 AKP24417.1
PA11P1_048	27629 - 28081	59.6	150	putative structural protein [Pseudomonas phage LMA2] structural protein [Pseudomonas phage phiKT28]	2E-103 2E-102	YP_002154264.1 AKJ71471.1
PA11P1_049	28081 - 28404	54.6	107	putative structural protein [Pseudomonas phage LMA2] putative structural protein [Pseudomonas phage JG024]	2E-75 5E-75	YP_002154265.1 YP_006200797.1
PA11P1_050	28401 - 28751	53.0	116	putative structural protein [Pseudomonas phage LMA2] structural protein [Pseudomonas phage SL1]	3E-78 1E-77	YP_002154266.1 AUS03345.1
PA11P1_051	28753 - 29184	64.1	143	hypothetical protein PPSN_gp35 [Pseudomonas phage SN] hypothetical protein PII10A_51 [Pseudomonas aeruginosa]	8E-93 2E-92	YP_002418841.1 SBT96733.1
PA11P1_052	29194 - 29697	52.2	167	structural protein [Pseudomonas phage SN] putative structural protein [Pseudomonas phage LMA2]	3E-115 1E-114	YP_002418842.1 YP_002154268.1
PA11P1_053	29697 - 30236	51.1	179	putative structural protein [Pseudomonas phage LMA2] putative structural protein [Pseudomonas phage LBL3]	5E-128 2E-127	YP_002154269.1 YP_002154178.1
PA11P1_054	30245 - 30838	46.8	197	putative structural protein [Pseudomonas phage KPP12] hypothetical protein vBPaeME217_00038 [Pseudomonas phage vB_PaeM_E217]	3E-140 2E-139	YP_007238190.1 ASZ72422.1
PA11P1_055	30848 - 31276	57.1	142	hypothetical protein LBL3_gp35 [Pseudomonas phage LBL3]	4E-101	YP_002154180.1

				hypothetical protein phiKTN6_037 [<i>Pseudomonas</i> phage phiKTN6]	2E-100	AKJ71569.1
PA11P1_056	31280 - 33856	58.2	858	putative lytic tail protein [<i>Pseudomonas</i> phage LMA2]	0	YP_002154272.1
				internal (core) protein [<i>Pseudomonas</i> phage NP3]	0	AMQ76156.1
PA11P1_057	33856 - 34719	52.1	287	putative structural protein [<i>Pseudomonas</i> phage LMA2]	0	YP_002154273.1
				putative structural protein [<i>Pseudomonas</i> phage vB_PaeM_CEB_DP1]	0	AKP24427.1
PA11P1_058	34719 - 35252	48.3	177	hypothetical protein PP141_gp41 [<i>Pseudomonas</i> phage 14-1]	2E-127	YP_002364349.1
				hypothetical protein [<i>Pseudomonas</i> phage DL68]	5E-127	YP_009215187.1
PA11P1_059	35308 - 35973	53	221	putative baseplate protein [<i>Pseudomonas</i> phage JG024]	5E-71	YP_006200807.1
				baseplate protein [<i>Pseudomonas</i> phage phiKTN6]	6E-71	AKJ71573.1
PA11P1_060A	35984 - 36037	42.6	17	hypothetical protein PB1_gp43 [<i>Pseudomonas</i> phage PB1]	3E-09	YP_002455973.1
				putative baseplate protein [<i>Pseudomonas</i> phage SN]	2E-04	YP_002418850.1
PA11P1_060B	36030 - 37283	57.8	417	putative baseplate protein [<i>Pseudomonas</i> phage NH-4]	0	YP_007002590.1
				hypothetical protein BrSP1_62 [<i>Pseudomonas</i> phage BrSP1]	0	ATI16244.1
PA11P1_061	37280 - 38794	55.7	504	hypothetical protein I7A_045 [<i>Pseudomonas</i> phage NH-4]	0	YP_007002591.1
				putative structural protein [<i>Pseudomonas</i> phage JG024]	0	YP_006200809.1
PA11P1_062	38799 - 41687	57.8	962	tail fibers protein [<i>Pseudomonas</i> phage NP3]	0	AMQ76163.1
				putative tail fiber component [<i>Pseudomonas</i> phage NH-4]	0	YP_007002592.1
PA11P1_063	41689 - 42117	58.3	142	hypothetical protein [<i>Pseudomonas</i> phage NP3]	4E-98	AMQ76164.1
				putative tail fiber component [<i>Pseudomonas</i> phage JG024]	6E-97	YP_006200811.1
PA11P1_064	42117 - 42779	60.5	220	lytic enzyme [<i>Pseudomonas</i> phage NP3]	2E-161	AMQ76165.1
				putative endolysin [<i>Pseudomonas</i> phage JG024]	7E-161	YP_006200812.1
PA11P1_065c	43054 - 42803	51.2	83	hypothetical protein PP141_gp48 [<i>Pseudomonas</i> phage 14-1]	2E-50	YP_002364356.1
				hypothetical protein LMA2_gp47 [<i>Pseudomonas</i> phage LMA2]	3E-50	YP_002154281.1
PA11P1_066c	44245 - 43334	56.6	303	DNA ligase [<i>Pseudomonas</i> phage phiKT28]	0	AKJ71489.1
				putative DNA ligase [<i>Pseudomonas</i> phage JG024]	0	YP_006200814.1
PA11P1_067c	44854 - 44300	54.4	184	DNA binding protein [<i>Pseudomonas</i> phage DL68]	2E-132	YP_009215178.1
				hypothetical protein PJG24_051 [<i>Pseudomonas</i> phage JG024]	2E-131	YP_006200815.1
PA11P1_068c	45456 - 44851	60.2	201	hypothetical protein ORF050 [<i>Pseudomonas</i> phage F8]	4E-139	YP_001294467.1
				hypothetical protein PP141_gp51 [<i>Pseudomonas</i> phage 14-1]	9E-139	YP_002364359.1
PA11P1_069c	46409 - 45510	59.9	299	hypothetical protein PP141_gp52 [<i>Pseudomonas</i> phage 14-1]	0	YP_002364360.1
				hypothetical protein [<i>Pseudomonas</i> phage DL68]	0	YP_009215176.1
PA11P1_070c	47118 - 46498	53.3	206	hypothetical protein vBPaeMLS1_79 [<i>Pseudomonas</i> phage vB_PaeM_LS1]	3E-145	AVJ48847.1
				hypothetical protein SL1_50 [<i>Pseudomonas</i> phage SL1]	1E-144	AUS03325.1
PA11P1_071c	48772 - 47213	55.1	519	hypothetical protein PPSN_gp55 [<i>Pseudomonas</i> phage SN]	0	YP_002418861.1
				DNA helicase [<i>Pseudomonas</i> phage vB_Pae436M-8]	0	ANT44241.1
PA11P1_072c	49179 - 48769	55.2	136	hypothetical protein LBL3_gp52 [<i>Pseudomonas</i> phage LBL3]	6E-95	YP_002154197.1
				hypothetical protein [<i>Pseudomonas</i> phage NP3]	6E-95	AMQ76173.1
PA11P1_073c	52279 - 49172	54.9	1035	hypothetical protein PP141_gp56 [<i>Pseudomonas</i> phage 14-1]	0	YP_002364364.1
				DNA polymerase III subunit alpha [<i>Pseudomonas</i> phage vB_Pae_PS44]	0	YP_009211383.1
PA11P1_074c	52833 - 52279	52.6	184	putative DNA polymerase III, epsilon subunit [<i>Pseudomonas</i> phage LMA2]	3E-135	YP_002154290.1
				putative DNA polymerase III epsilon subunit [<i>Pseudomonas</i> phage NH-4]	3E-135	YP_007002604.1
PA11P1_075c	53940 - 52909	58.4	343	putative 3'-phosphatase, 5'-polynucleotide kinase [<i>Pseudomonas aeruginosa</i>]	0	SBT96767.1
				putative polynucleotide kinase [<i>Pseudomonas</i> phage KPP12]	0	YP_007238211.1

PA11P1_076c	54134 - 53943	48.4	63	hypothetical protein PJG24_060 [<i>Pseudomonas</i> phage JG024] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	3E-35 1E-34	YP_006200824.1 YP_007238212.1
PA11P1_077c	55053 - 54136	58.6	305	putative thymidylate synthase [<i>Pseudomonas</i> phage JG024] hypothetical protein PP141_gp60 [<i>Pseudomonas</i> phage 14-1]	0 0	YP_006200825.1 YP_002364368.1
PA11P1_078c	55259 - 55053	51.2	68	hypothetical protein [<i>Pseudomonas</i> phage KPP12] hypothetical protein SL1_42 [<i>Pseudomonas</i> phage SL1]	4E-41 8E-41	YP_007238214.1 AUS03317.1
PA11P1_079c	55533 - 55267	56.9	88	hypothetical protein [<i>Pseudomonas</i> phage PA5] hypothetical protein phiKT28_064 [<i>Pseudomonas</i> phage phiKT28]	2E-56 5E-56	APD20761.1 AKJ71502.1
PA11P1_080c	55751 - 55533	55.7	72	hypothetical protein PPSN_gp64 [<i>Pseudomonas</i> phage SN] hypothetical protein LMA2_gp62 [<i>Pseudomonas</i> phage LMA2]	2E-46 3E-46	YP_002418870.1 YP_002154296.1
PA11P1_081c	55953 - 55735	59.8	72	hypothetical protein LBL3_gp61 [<i>Pseudomonas</i> phage LBL3] hypothetical protein [<i>Pseudomonas</i> phage KPP12]	5E-43 2E-42	YP_002154206.1 YP_007238217.1
PA11P1_082c	56183 - 55953	59.7	76	hypothetical protein PP141_gp65 [<i>Pseudomonas</i> phage 14-1] hypothetical protein LBL3_gp62 [<i>Pseudomonas</i> phage LBL3]	6E-50 1E-49	YP_002364373.1 YP_002154207.1
PA11P1_083c	57272 - 56271	56.2	333	hypothetical protein [<i>Pseudomonas</i> phage NP3] hypothetical protein PPSN_gp67 [<i>Pseudomonas</i> phage SN]	0 0	AMQ76184.1 YP_002418873.1
PA11P1_084c	58117 - 57377	61.7	246	hypothetical protein [<i>Pseudomonas</i> phage NP3] putative structural protein [<i>Pseudomonas</i> phage LMA2]	2E-161 4E-94	AMQ76185.1 YP_002154300.1
PA11P1_085c	59466 - 58279	55.3	395	hypothetical protein LBL3_gp65 [<i>Pseudomonas</i> phage LBL3] putative ATP-dependent exonuclease V [<i>Pseudomonas</i> phage SN]	0 0	YP_002154210.1 YP_002418875.1
PA11P1_086c	59,875 - 59453	56.7	140	hypothetical protein ORF068 [<i>Pseudomonas</i> phage F8] hypothetical protein [<i>Pseudomonas</i> phage NP3]	3E-98 1E-97	YP_001294485.1 AMQ76187.1
PA11P1_087	60044 - 60829	58.8	261	hypothetical protein ORF069 [<i>Pseudomonas</i> phage F8] hypothetical protein PPSN_gp71 [<i>Pseudomonas</i> phage SN]	0 0	YP_001294486.1 YP_002418877.1
PA11P1_088	60840 - 62063	59.1	407	hypothetical protein vBPaeME215_00050 [<i>Pseudomonas</i> phage vB_PaeM_E215] hypothetical protein LBL3_gp68 [<i>Pseudomonas</i> phage LBL3]	0 0	ASZ72528.1 YP_002154213.1
PA11P1_089	62087 - 62536	58.2	149	hypothetical protein PP141_gp72 [<i>Pseudomonas</i> phage 14-1] hypothetical protein [<i>Pseudomonas</i> phage NP3]	3E-105 5E-105	YP_002364380.1 AMQ76190.1
PA11P1_090	62533 - 63609	57.5	358	hypothetical protein [<i>Pseudomonas</i> phage DL52] hypothetical protein PP141_gp73 [<i>Pseudomonas</i> phage 14-1]	0 0	AKF13701.1 YP_002364381.1
PA11P1_091	63615 - 63800	47.8	61	hypothetical protein ORF073 [<i>Pseudomonas</i> phage F8] hypothetical protein phiKT28_076 [<i>Pseudomonas</i> phage phiKT28]	3E-33 3E-32	YP_001294490.1 AKJ71514.1
PA11P1_092	63948 - 65687	53.3	579	putative Ploop ATPase [<i>Pseudomonas aeruginosa</i>] virulence-associated protein E [<i>Pseudomonas</i> phage vB_Pae_PS44]	0 0	SBT96795.1 YP_009211402.1

Table S7: Summarized results of the host range screenings. See also Fig. S1 for details.

<i>Pseudomonas aeruginosa</i> strain access number	PA1P1	PA8P1	PA11P1	fHo-Pae01
5513	+	-	-	-
5514	+/-	-	+/-	-
5525	+	+	+	+
5537	+	+/-	+	-
5538	-	-	-	-
5539	+	+/-	+	+/-

5548	-	-	-	-
5550	+	+	+	+
5551	-	-	-	-
5553	-	-	-	-
5668	+	+/-	+/-	-
5669	+	+	+	+
5670	+/-	-	+/-	-
5671	+	+	+	+
5672	+	+	+	+/-
5740	-	-	-	-
5741	+	+	+	+
5742	+	-	+	-
5743	+	+	+	+
5745	+	+	+	+
5746	+	-	+	-
5747	+	+	+	-
5826	+	+	+	+
5827	+	+	+	+
5828	+	+	+	+/-
5829	+/-	-	+	-
5831	+	+	+	-
5832	-	-	-	-
5833	+	+	+	+
5834	+	+	+	+
5835	+	+	+	+
5836	+	+	+	-
5837	+	+	+	+/-
5838	+	+	+	-
5839	+	+	+	-
5840	-	-	-	-
5841	-	-	-	-
5842	-	-	-	-
5844	-	-	-	-
5845	-	-	-	-
5846	+	+	+	+
5847	+	-	+	-
5848	+	-	+/-	+/-
PA1 (6327)	+	+/-	+	-
PA8 (6329)	+	+	+	+
PA11 (6331)	+	+	+	-
6663	+	+	+	-

In each well, 190 μ l of 1:40 dilution of the host bacteria overnight culture was mixed with 10 μ l lysate (10^9 pfu/ml) of one of the phages.

+ : infection was observed, - : no infection, +/- : partial infection

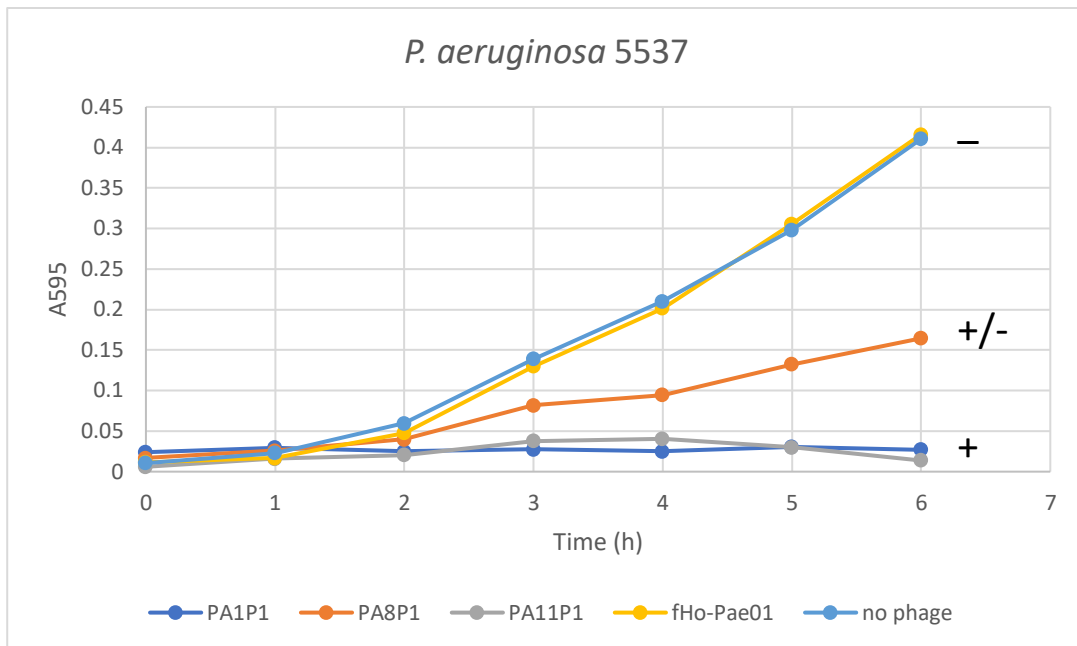


Fig. S1. A representative image of the evaluation of the host range screening results in Table S5. + : infection was observed, - : no infection, +/- : partial infection.

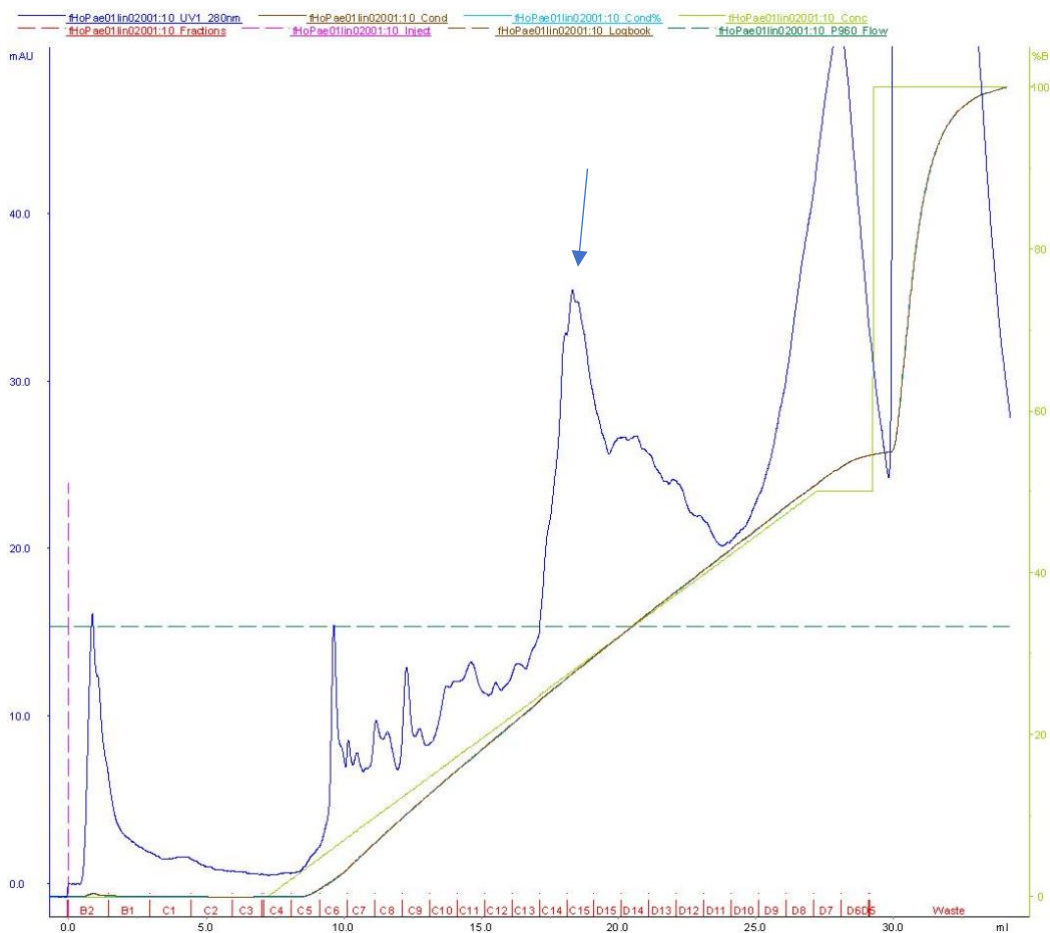


Fig. S2. Linear gradient purification of phage fHo-Pae01. The peak predicted to contain the phage is indicated with an arrow. Buffer A (20 mM Tris-Cl, pH 8.5), buffer B (20 mM Tris-Cl, 1M NaCl, pH 8.5)

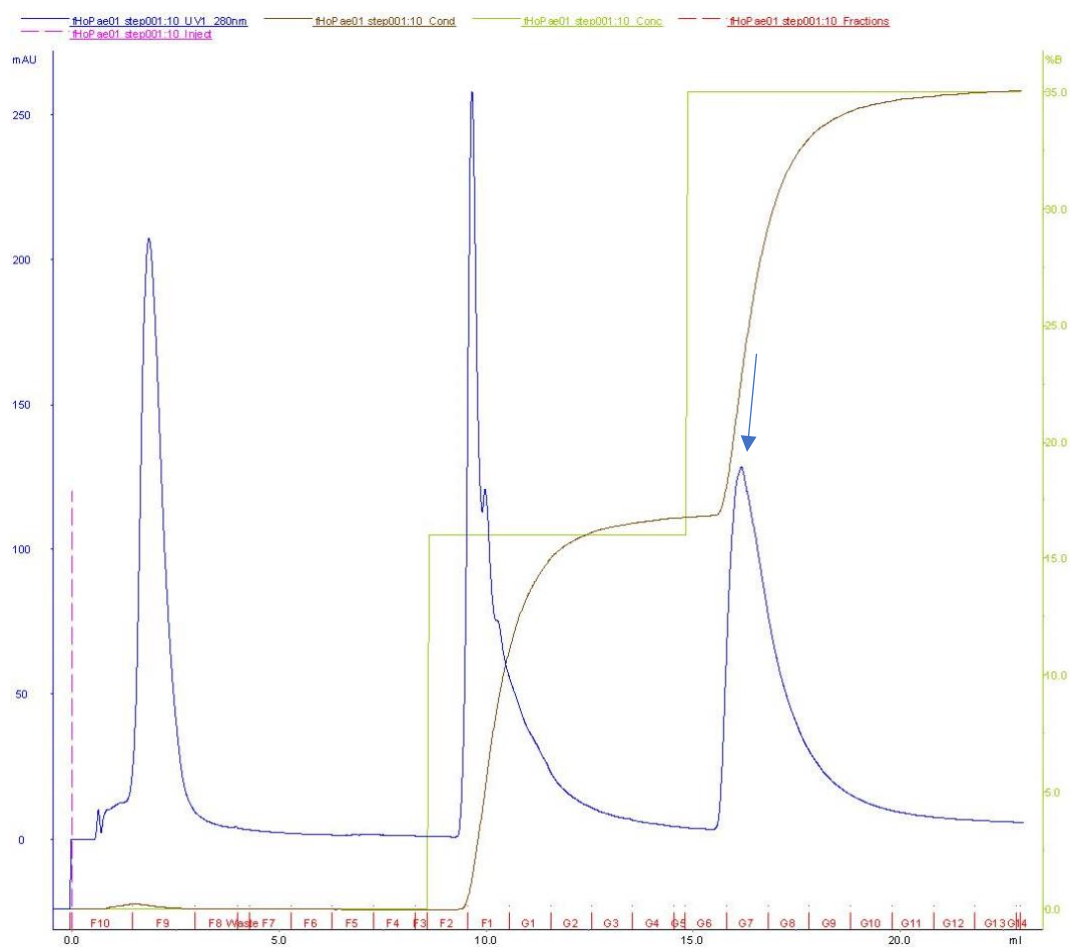


Fig. S3. Step-gradient purification of phage fHo-Pae01. The peak predicted to contain the phage is indicated with an arrow. Fractions G7 and G8 were harvested. Buffer A: 20 mM Tris-Cl, pH 8.5; buffer B: 20 mM Tris-Cl, 1M NaCl, pH 8.5.

References

Mattila S, Ruotsalainen P, Jalasvuori M. On-demand isolation of bacteriophages against drug-resistant bacteria for personalized phage therapy. *Frontiers in Microbiology* 2015 Nov 13;6.